

Human DNase I

LOCUS HUMDNASEI 1039 bp mRNA PRI 06-MAR-1995
 DEFINITION Human DNase I mRNA, complete cds.
 ACCESSION M55983
 VERSION M55983.1 GI:181623
 KEYWORDS DNase I.
 SOURCE Human pancreas, cDNA to mRNA.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1039)
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672

FEATURES Location/Qualifiers
 source 1..1039
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="hDNase-18-1"
 /tissue_type="pancreas"
 sig_peptide 160..225
 /gene="DNase I"
 CDS 160..1008
 /gene="DNase I"
 /codon_start=1
 /product="DNase I"
 /protein_id="AAA63170.1"
 /db_xref="GI:181624"
 /translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV
 SYIVQILSRVDIALVQEVDRSHLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERY
 LFVYRPDQVSAVDSYDDGCEPCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPG
 DAVAEIDALYDVYLDVQEKWGLEDMVLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLI
 PDSADTTATPTHCAYDRIVVAGMLLRGAVVPDSALPFNFQAAAYGLSDQLAQAI SDHYP
 VEVMK"
 gene 160..1008
 /gene="DNase I"
 mat_peptide 226..1005
 /gene="DNase I"
 /product="DNase I"

BASE COUNT 226 a 305 c 282 g 226 t
 ORIGIN

```

1 tcctgcacag gcagtgcctt gaagtgcctt ttcagagacc tttcttcata gactactttt
61 ttttctttaa gcagcaaaaag gagaaaattg tcatcaaaagg atattccaga ttcttgacag
121 cattctcgtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg
181 ggggcgctgc tggcactggc ggccctactg cagggggccg tgccctgaa gatcgagcc
241 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt
301 gtgcagatcc tgagccgcta tgacatgcc ctggtccagg aggtcagaga cagccacctg
361 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac
421 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg
481 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg
541 aacgacacct tcaaccgaga gccagccatt gtcagggttct tctcccgtt cagagaggtc
601 agggagtttg ccattgttcc cctgcagcgc gccccggggg acgcagtagc cgagatcgac
661 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgtcatgttg
721 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc
781 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca
841 cccacgcact gtgcctatga caggatcgtg gttgcaggga tgctgctccg aggcgcggtt
901 gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg
961 gcccaagcca tcagtgaaca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc
1021 cacaccagtt gaactgcag
```

//

Fig. 1

Human DNase I construct

LOCUS MHDNASE.DN 783 bp mRNA PRI 06-MAR-1995

DEFINITION Human DNase I mRNA, complete cds, Mature sequence modified to remove NarI site

ACCESSION M55983

NID g181623

KEYWORDS DNase I.

SOURCE Human pancreas, cDNA to mRNA.

ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1039)

AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.

TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis sputum

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)

MEDLINE 91067672

FEATURES

	Location/Qualifiers
source	1..1039 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="hDNase-18-1" /tissue_type="pancreas"
sig_peptide	160..225 /gene="DNase I"
CDS	160..1008 /gene="DNase I" /codon_start=1 /product="DNase I" /db_xref="PID:g181624" /translation="LKIAAFNIQTFGETKMSNATLVSYIVQILSRDYDIALVQEVDRSH LTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERYLFVYRPDQVSAVDSYYDDGCE PCGNDTFNREPAIVRFFSRFTEVREFAIVPLHAAPGDAVAEIDALYDVYLDVQEKWGL EDVMLMGDFNAGCSYVRPSQWSSIRLWTSPTFQWLIPDSADTTATPTHCAYDRIVVAG MLLRGAVVPDSALPFNFQAAYGLSDQLAQAI SDHYPVEVMLK"
gene	160..1008 /gene="DNase I"
mat_peptide	226..1005 /gene="DNase I" /product="DNase I"

BASE COUNT 168 a 236 c 220 g 159 t

ORIGIN

```

1 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
61 CTCGTCAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
121 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
181 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
241 CTGTTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
301 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTGTC GTTCTTCTCC
361 CGGTTACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGACGCA
421 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
481 GAGGACGTCA TGTGTATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCAG
541 TGGTCATCCA TCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
601 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
661 CTCCGAGGGG CCGTTGTTCC GCACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
721 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
781 TGA

```

//

Fig. 2(A)

LOCUS PAS155_GB. 858 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

frag 10..75

frag <10..>75

source <10..>75

sig_peptide 10..75

CDS 10..>75

Location/Qualifiers

/note="160 to 225 of Untitled1"

/note="1 to 1039 of M55983.DNA [Split]"

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="hDNase-18-1"

/tissue_type="pancreas [Split]"

/gene="DNase I"

/codon_start="1"

/product="DNase I"

/db_xref="PID:g181624"

/translation="MRGMKLLGALLALAALLQGAVSLKIAAFNIQTFGETKMSNATLV

SYIVQILSRVDIALVQEVDRDHLTAVGKLLDNLNQDAPDTYHYVVSEPLGRNSYKERY

LFVYRPDQVSAVDSYYYDDGCEPCGNDFNREPAIVRFFSRFTEVREFAIIVPLHAAPG

D... [Split]"

gene 10..>75

frag 76..858

frag 76..858

frag join(76..>129,<131..147)

frag join(76..>126,<127..>129,<131..147)

frag join(76..>126,<127..>129,<131..147)

BASE COUNT 177 A 260 C 251 G 170 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGAGGGGCAT GAAGCTGCTG GGGGCGCTGC TGGCACTGGC GGCCCTACTG

61 CAGGGGGCCG TGTCCCTGAA GATCGCAGCC TTCAACATCC AGACATTTGG GGAGACCAAG

121 ATGTCCAATG CCACCCTCGT CAGCTACATT GTGCAGATCC TGAGCCGCTA CGACATCGCC

181 CTGGTCCAGG AGGTCAGAGA CAGCCACCTG ACTGCCGTGG GGAAGCTGCT GGACAACCTC

241 AATCAGGACG CACCAGACAC CTATCACTAC GTGGTCAGTG AGCCACTGGG ACGGAACAGC

301 TATAAGGAGC GCTACCTGTT CGTGTACAGG CCTGACCAGG TGTCTGCGGT GGACAGCTAC

361 TACTACGATG ATGGCTGCGA GCCCTGCGGG AACGACACCT TCAACCGAGA GCCAGCCATT

421 GTCAGGTTCT TCTCCCGGTT CACAGAGGTC AGGGAGTTTG CCATTGTTCC CCTGCATGCG

481 GCCCCGGGGG ACGCAGTAGC CGAGATCGAC GCTCTCTATG ACGTCTACCT GGATGTCCAA

541 GAGAAATGGG GCTTGGAGGA CGTCATGTTG ATGGGCGACT TCAATGCGGG CTGCAGCTAT

601 GTGAGACCCT CCCAGTGGTC ATCCATCCGC CTGTGGACAA GCCCCACCTT CCAGTGGCTG

661 ATCCCCGACA GCGCTGACAC CACAGCTACA CCCACGCACT GTGCCTATGA CAGGATCGTG

721 GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT GTTCCCGACT CGGCTCTTCC CTTTAACTTC

781 CAGGCTGCCT ATGGCCTGAG TGACCAACTG GCCCAAGCCA TCAGTGACCA CTATCCAGTG

841 GAGGTGATGC TGAAGTGA

//

Fig. 2(B)

pAS6 – light chain

LOCUS HMFG1LC2.D 721 bp DNA
 DEFINITION HUMANISED HMFG1 LIGHT CHAIN Vnp LEADER.
 ACCESSION _____
 KEYWORDS _____
 SOURCE _____
 ORGANISM _____
 REFERENCE 1 (BASES 1 TO 342)
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 ETC
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT SCANNED IN FROM JOURNAL
 FEATURES _____
 SITES _____

18-AUG-1998

This is the sequence of the HMFG1 light chain gene with the
 Vnp leader sequence attached. Translate from
 residue 1. Note residue 399 is T > A in all clones leading
 to R133 silent mutation (T in Verhoeyen paper)

BASE COUNT 197 a 202 c 182 g 140 t
 ORIGIN ?

	x LEADER SEQ							
1	ATGGGATGGA	GCTGTATCAT	CCTCTTCTTG	GTAGCAACAG	CTACAGGTGT	CCACTCGGAC		
61	ATCCAGATGA	CCCAGAGCCC	AAGCAGCCTG	AGCGCCAGCG	TGGGTGACAG	AGTGACCATC		
121	ACCTGTAAGT	CCAGTCAGAG	CCTTTTATAT	AGTAGCAATC	AAAAGATCTA	CTTGCCCTGG		
181	TACCAGCAGA	AGCCAGGTAA	GGCTCCAAAG	CTGCTGATCT	ACTGGGCATC	CACTAGGGAA		
241	TCTGGTGTGC	CAAGCAGATT	CAGCGGTAGC	GGTAGCGGTA	CCGACTTCAC	CTTCACCATC		
301	AGCAGCCTCC	AGCCAGAGGA	CATCGCCACC	TACTACTGCC	AGCAATATTA	TAGATATCCT		
361	CGGACGTTTC	GCCAAGGGAC	CAAGGTGGAA	ATCAAACGAA	CTGTGGCTGC	ACCATCTGTC		
421	TTCATCTTCC	CGCCATCTGA	TGAGCAGTTG	AAATCTGGAA	CTGCCTCTGT	TGTGTGCCTG		
481	CTGAATAACT	TCTATCCCAG	AGAGGCCAAA	GTACAGTGGA	AGGTGGATAA	CGCCCTCCAA		
541	TCGGGTAACT	CCCAGGAGAG	TGTCACAGAG	CAGGACAGCA	AGGACAGCAC	CTACAGCCTC		
601	AGCAGCACCC	TGACGCTGAG	CAAAGCAGAC	TACGAGAAAC	ACAAAGTCTA	CGCCTGCGAA		
661	GTCACCCATC	AGGGCCTGAG	CTCGCCCGTC	ACAAAGAGCT	TCAACAGGGG	AGAGTGTTAG		
721	A							

//

Fig. 3(A)

LOCUS HHMFG1KLC_ 730 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag 10..730

/note="1 to 721 of hHMFG1light chain"

frag 10..730

/note="1 to 72 of 104linker"

frag join(10..>63,<65..81)

/note="1 to 72 of 103linker [Split]"

frag join(10..>60,<61..>63,<65..81)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 198 A 208 C 184 G 140 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC

61 CACTCCGACA TCCAGATGAC CCAGAGCCCA AGCAGCCTGA GCGCCAGCGT GGGTGACAGA

121 GTGACCATCA CCTGTAAGTC CAGTCAGAGC CTTTTATATA GTAGCAATCA AAAGATCTAC

181 TTGGCCTGGT ACCAGCAGAA GCCAGGTAAG GCTCCAAAGC TGCTGATCTA CTGGGCATCC

241 ACTAGGGAAT CTGGTGTGCC AAGCAGATTC AGCGGTAGCG GTAGCGGTAC CGACTTCACC

301 TTCACCATCA GCAGCCTCCA GCCAGAGGAC ATCGCCACCT ACTACTGCCA GCAATATTAT

361 AGATATCCTC GGACGTTCGG CCAAGGGACC AAGGTGGAAA TCAAACGAAC TGTGGCTGCA

421 CCATCTGTCT TCATCTTCCC GCCATCTGAT GAGCAGTTGA AATCTGGAAC TGCCTCTGTT

481 GTGTGCCTGC TGAATAACTT CTATCCCAGA GAGGCCAAG TACAGTGGAA GGTGGATAAC

541 GCCCTCCAAT CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC

601 TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA CAAAGTCTAC

661 GCCTGCGAAG TCACCCATCA GGCCTGAGC TCGCCCGTCA CAAAGAGCTT CAACAGGGGA

721 GAGTGTTAGA

//

Fig. 3(B)

[illegible]

Figure 1 consists of three bar charts. The first chart shows the percentage of respondents who answered 'No' to the question 'Do you have a job?'. The second chart shows the percentage of respondents who answered 'Yes' to the same question. The third chart shows the percentage of respondents who answered 'Don't know' to the same question. The y-axis for all charts ranges from 0 to 100. The x-axis for all charts shows the three age groups: 18-24, 25-34, and 35-44.

Age Group	No (%)	Yes (%)	Don't know (%)
18-24	~10	~90	~0
25-34	~10	~90	~0
35-44	~10	~90	~0

pAS6 – heavy chain

LOCUS HHMFG1HC.D 1404 bp DNA
 DEFINITION HUMANISED HMFG1 heavy chain
 ACCESSION HHMFG1H
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT VH domain SCANNED IN FROM JOURNAL
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 333 a 439 c 379 g 253 t
 ORIGIN ?

← LEADER

```

1  ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GCGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA ATGA
  
```

Antibody DNase Fusions Made Here
(eg pAS34----39.)

→ End of lower hinge region of heavy chain. PAPE Amino
Acid Seq. Fab'₂ fusions were made at this point.

Those with HYBRID HINGES are altered further
up

→ This part GACAAAAC
 D K T H T

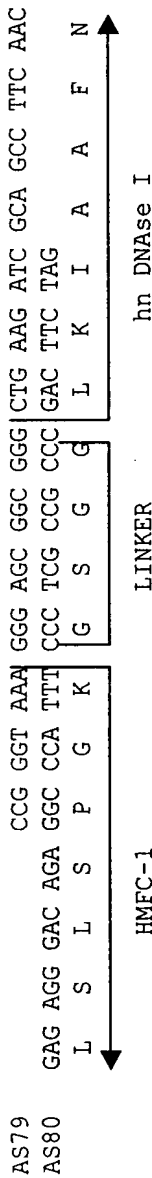
After this sequence you get the HYBRID HINGE + LINKER SEQUENCES
Then DNase I (eg Fab-DNase construct pAS302)

Fig. 3(D)

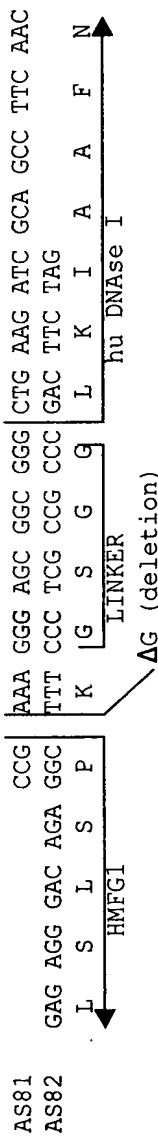
Fig. 4(A)

Oligos involved in the fusion of whole antibody-DNase

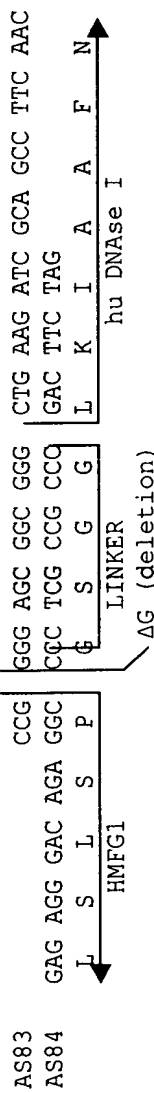
Constructs pAS34/37



Constructs pAS35/38

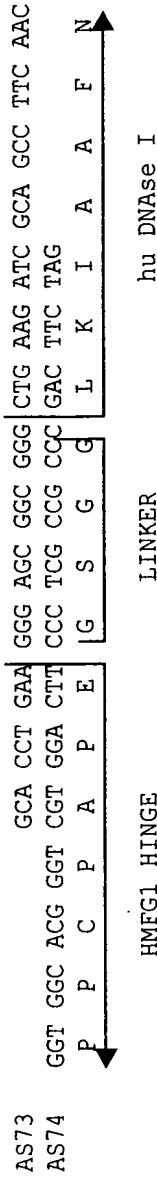


Constructs pAS36/39



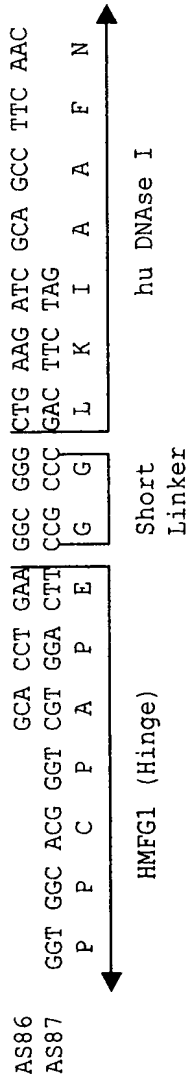
Oligos involved in the fusion of Fab'2-DNaseI

Constructs pAS23/27

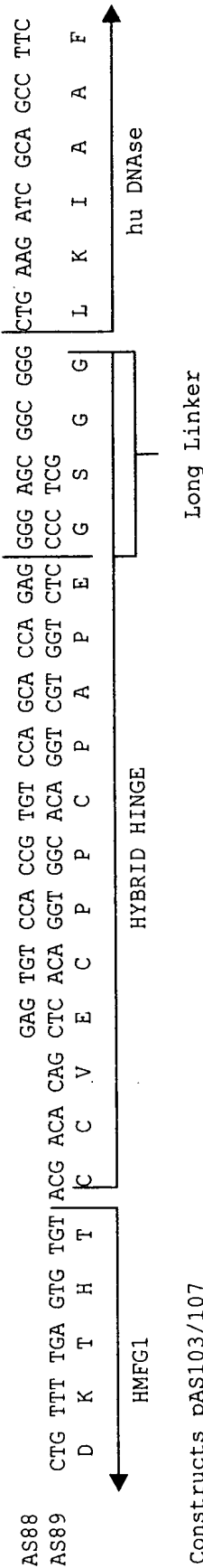


Oligos involved in the fusion of new Fab'2-DNaseI molecules (5.7.99)

Constructs pAS101/105



Constructs pAS102/106



Constructs pAS103/107

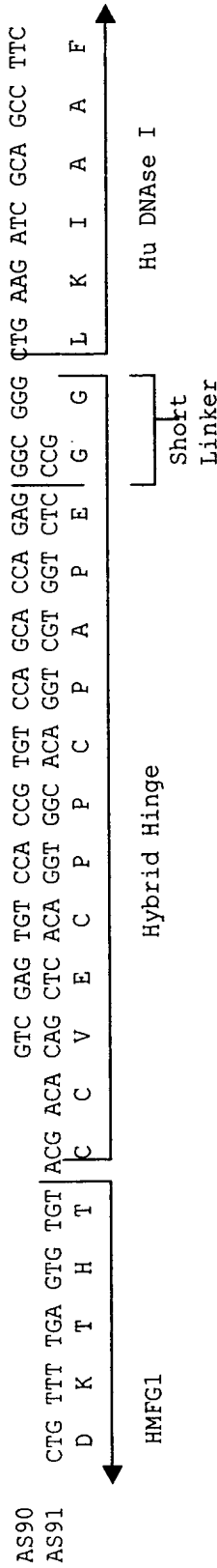


Fig. 4(B)

pAS23

LOCUS PAS23.DNA 1554 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (construct 1)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic
 fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 344 a 468 c 434 g 308 t
 ORIGIN

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAG GGAGCGGCGG GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCCTCTC CCGGTTTACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTC CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGGAGG TGATGCTGAA GTGA

```

//

Fig. 5(A)

25-AUG-2000

LOCUS FDDNASE23_ 1554 BP SS-DNA SYN

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

frag Location/Qualifiers
join(1..>720,<787..1554)
/note="1 to 1554 of 23.dna [Split]"

frag 721..786
/note="1 to 66 of 23/27linker"

frag join(721..>735,<736..786)
/note="1 to 78 of 102linker [Split]"

BASE COUNT 344 A 466 C 435 G 309 T 0 OTHER

ORIGIN

1	ATGGGATGGA	GCTGTATCAT	CCTCTTCTTG	GTAGCAACAG	CTACAGGTGT	CCACTCCCAG
61	GTGCAGCTGG	TGCAGTCTGG	GGCAGAGGTG	AAAAAGCCTG	GGGCCTCAGT	GAAGGTGTCC
121	TGCAAGGCTT	CTGGCTACAC	CTTCAGTGCC	TACTGGATAG	AGTGGGTGCG	CCAGGCTCCA
181	GGAAAGGGCC	TCGAGTGGGT	CGGAGAGATT	TTACCTGGAA	GTAATAATTC	TAGATAACAAT
241	GAGAAGTTCA	AGGGCCGAGT	GACAGTCACT	AGAGACACAT	CCACAAACAC	AGCCTACATG
301	GAGCTCAGCA	GCCTGAGGTC	TGAGGACACA	GCCGTCTATT	ACTGTGCAAG	ATCCTACGAC
361	TTTGCTGGT	TTGCTTACTG	GGGCCAAGGG	ACTCTGGTCA	CAGTCTCCTC	AGCCTCCACC
421	AAGGGCCCCAT	CGGTCTTCCC	CCTGGCACCC	TCCTCCAAGA	GCACCTCTGG	GGGCACAGCG
481	GCCCTGGGCT	GCCTGGTCAA	GGACTACTTC	CCCGAACCGG	TGACGGTGTC	GTGGAACTCA
541	GGCGCCCTGA	CCAGCGGCGT	GCACACCTTC	CCGGCTGTCC	TACAGTCCTC	AGGACTCTAC
601	TCCCTCAGCA	GCGTGGTGAC	CGTGCCCTCC	AGCAGCTTGG	GCACCCAGAC	CTACATCTGC
661	AACGTGAATC	ACAAGCCCAG	CAACACCAAG	GTGGACAAGA	AAGTTGAGCC	CAAATCTTGT
721	GACAAAACCTC	ACACATGTCC	ACCGTGTCCA	GCACCAGAGG	GGAGCGGCGG	GCTGAAGATC
781	GCAGCCTTCA	ACATCCAGAC	ATTTGGGGAG	ACCAAGATGT	CCAATGCCAC	CCTCGTCAGC
841	TACATTGTGC	AGATCCTGAG	CCGCTACGAC	ATCGCCCTGG	TCCAGGAGGT	CAGAGACAGC
901	CACCTGACTG	CCGTGGGGAA	GCTGCTGGAC	AACCTCAATC	AGGACGCACC	AGACACCTAT
961	CACTACGTGG	TCAGTGAGCC	ACTGGGACGG	AACAGCTATA	AGGAGCGCTA	CCTGTTTCGTG
1021	TACAGGCCCTG	ACCAGGTGTC	TGCGGTGGAC	AGCTACTACT	ACGATGATGG	CTGCGAGCCC
1081	TGCGGGAACG	ACACCTTCAA	CCGAGAGCCA	GCCATTGTCA	GGTTCCTTCTC	CCGGTTTACA
1141	GAGGTCAGGG	AGTTTGCCAT	TGTTCCCCTG	CATGCGGCCC	CGGGGGACGC	AGTAGCCGAG
1201	ATCGACGCTC	TCTATGACGT	CTACCTGGAT	GTCCAAGAGA	AATGGGGCTT	GGAGGACGTC
1261	ATGTTGATGG	GCGACTTCAA	TGCGGGCTGC	AGCTATGTGA	GACCCTCCA	GTGGTCATCC
1321	ATCCGCTGT	GGACAAGCCC	CACCTTCCAG	TGGCTGATCC	CCGACAGCGC	TGACACCACA
1381	GCTACACCCA	CGCACTGTGC	CTATGACAGG	ATCGTGTTG	CAGGGATGCT	GCTCCGAGGG
1441	GCCGTTGTTC	CCGACTCGGC	TCTTCCCTTT	AACTTCCAGG	CTGCCTATGG	CCTGAGTGAC
1501	CAACTGGCCC	AAGCCATCAG	TGACCACTAT	CCAGTGAGG	TGATGCTGAA	GTGA

//

Fig. 5(B)

LOCUS FDDNASE23K 1563 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -

FEATURES Location/Qualifiers
 frag 10..1563
 /note="1 to 1554 of FdDNase23correct"
 frag join(10..>729,<796..1563)
 /note="1 to 1554 of 23.dna [Split]"
 frag 730..795
 /note="1 to 66 of 23/27linker"
 frag join(730..>744,<745..795)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 345 A 472 C 437 G 309 T 0 OTHER
 ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG
 541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAAAACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
 781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
 841 CTCGTACGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
 901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
 961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
 1021 CTGTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
 1081 TGCGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCAG GTTCTTCTCC
 1141 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
 1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 1261 GAGGACGTCA TGTTGATGGG GACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCAG
 1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
 1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
 1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCCTTTA ACTTCCAGGC TGCCTATGGC
 1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
 1561 TGA

//

Fig. 5(C)

5'		9		18		27		36		45		54						
	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GCT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
		63		72		81		90		99		108						
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
		117		126		135		144		153		162						
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
		171		180		189		198		207		216						
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
		225		234		243		252		261		270						
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
		279		288		297		306		315		324						
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
		333		342		351		360		369		378						
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
		387		396		405		414		423		432						
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
		441		450		459		468		477		486						
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
		495		504		513		522		531		540						
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
		549		558		567		576		585		594						
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

Fig. 5(D)
(Sheet 1 of 3)

		603				612				621				630				639				648			
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q								
		657				666				675				684				693				702			
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K								
		711				720				729				738				747				756			
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P								
		765				774				783				792				801				810			
GAA	GGG	AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
E	G	S	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E								
		819				828				837				846				855				864			
ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
T	K	M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R								
		873				882				891				900				909				918			
TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
Y	D	I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G								
		927				936				945				954				963				972			
AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
K	L	L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V								
		981				990				999				1008				1017				1026			
AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
S	E	P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R								
		1035				1044				1053				1062				1071				1080			
CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P								
		1089				1098				1107				1116				1125				1134			
TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG								
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---								
C	G	N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R								
		1143				1152				1161				1170				1179				1188			
TTC	ACA	GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC								
---	---	---	---																						

Fig. 5(D)
(Sheet 2 of 3)



GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA

A V A E I D A L Y D V Y L D V Q E K

1251 1260 1269 1278 1287 1296
TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT

W G L E D V M L M G D F N A G C S Y

1305 1314 1323 1332 1341 1350
GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG

V R P S Q W S S I R L W T S P T F Q

1359 1368 1377 1386 1395 1404
TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT

W L I P D S A D T T A T P T H C A Y

1413 1422 1431 1440 1449 1458
GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG

D R I V V A G M L L R G A V V P D S

1467 1476 1485 1494 1503 1512
GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA

A L P F N F Q A A Y G L S D Q L A Q

1521 1530 1539 1548
GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

A I S D H Y P V E V M L K *

Fig. 5(D)
(Sheet 3 of 3)

pAS27

LOCUS PAS27.DNA 1584 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS(construct 1)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 354 a 474 c 446 g 310 t
ORIGIN

```
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCC ACCGTGCCCA GCACCTGAAG GGAGCGGCGG GCTGAAGATC
781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC
841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC
901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT
961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG
1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC
1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCCTCTC CCGGTTTACA
1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG
1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC
1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC
1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA
1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGGTTG CAGGGATGCT GCTCCGAGGG
1441 GCCGTTGTTT CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC
1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCAGTGAGAG TGATGCTGAA GGGGGGCGGA
1561 CCCAAAAAGA AGCGCAAGGT TTGA
```

//

Fig. 6(A)

12 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

LOCUS FDDNASE27_ 1584 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

Location/Qualifiers

frag join(1..>720,<787..1584)

/note="1 to 1584 of 27.dna [Split]"

frag 721..786

/note="1 to 66 of 23/27linker"

frag join(721..>735,<736..786)

/note="1 to 78 of 102linker [Split]"

BASE COUNT 354 A 472 C 447 G 311 T 0 OTHER

ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC

121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA

181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT

241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG

301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC

361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC

421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG

481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTA

541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC

601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC

661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT

721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAGAGG GGAGCGGCGG GCTGAAGATC

781 GCAGCCTTCA ACATCCAGAC ATTTGGGGAG ACCAAGATGT CCAATGCCAC CCTCGTCAGC

841 TACATTGTGC AGATCCTGAG CCGCTACGAC ATCGCCCTGG TCCAGGAGGT CAGAGACAGC

901 CACCTGACTG CCGTGGGGAA GCTGCTGGAC AACCTCAATC AGGACGCACC AGACACCTAT

961 CACTACGTGG TCAGTGAGCC ACTGGGACGG AACAGCTATA AGGAGCGCTA CCTGTTCGTG

1021 TACAGGCCTG ACCAGGTGTC TGCGGTGGAC AGCTACTACT ACGATGATGG CTGCGAGCCC

1081 TGCGGGAACG ACACCTTCAA CCGAGAGCCA GCCATTGTCA GGTTCTTCTC CCGGTTTACA

1141 GAGGTCAGGG AGTTTGCCAT TGTTCCCCTG CATGCGGCCC CGGGGGACGC AGTAGCCGAG

1201 ATCGACGCTC TCTATGACGT CTACCTGGAT GTCCAAGAGA AATGGGGCTT GGAGGACGTC

1261 ATGTTGATGG GCGACTTCAA TGCGGGCTGC AGCTATGTGA GACCCTCCCA GTGGTCATCC

1321 ATCCGCCTGT GGACAAGCCC CACCTTCCAG TGGCTGATCC CCGACAGCGC TGACACCACA

1381 GCTACACCCA CGCACTGTGC CTATGACAGG ATCGTGTTG CAGGGATGCT GCTCCGAGGG

1441 GCCGTTGTTT CCGACTCGGC TCTTCCCTTT AACTTCCAGG CTGCCTATGG CCTGAGTGAC

1501 CAACTGGCCC AAGCCATCAG TGACCACTAT CCACTGGAGG TGATGCTGAA GGGGGGCGGA

1561 CCAAAAAGA AGCGCAAGGT TTGA

//

Fig. 6(B)

LOCUS FDDNASE27K 1593 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -

FEATURES Location/Qualifiers
 frag 10..1593
 /note="1 to 1584 of FdDNase27correct"
 frag join(10..>729,<796..1593)
 /note="1 to 1584 of 27.dna [Split]"
 frag 730..795
 /note="1 to 66 of 23/27linker"
 frag join(730..>744,<745..795)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 355 A 478 C 449 G 311 T 0 OTHER
 ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG
 541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCTCTCA
 601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTTG ACAAACCTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG GAGCGGCGGG
 781 CTGAAGATCG CAGCCTTCAA CATCCAGACA TTTGGGGAGA CCAAGATGTC CAATGCCACC
 841 CTCGTCTAGCT ACATTGTGCA GATCCTGAGC CGCTACGACA TCGCCCTGGT CCAGGAGGTC
 901 AGAGACAGCC ACCTGACTGC CGTGGGGAAG CTGCTGGACA ACCTCAATCA GGACGCACCA
 961 GACACCTATC ACTACGTGGT CAGTGAGCCA CTGGGACGGA ACAGCTATAA GGAGCGCTAC
 1021 CTGTTTCGTGT ACAGGCCTGA CCAGGTGTCT GCGGTGGACA GCTACTACTA CGATGATGGC
 1081 TGCAGAGCCCT GCGGGAACGA CACCTTCAAC CGAGAGCCAG CCATTGTCTAG GTTCTTCTCC
 1141 CGGTTCACAG AGGTCAGGGA GTTTGCCATT GTTCCCCTGC ATGCGGCCCC GGGGGACGCA
 1201 GTAGCCGAGA TCGACGCTCT CTATGACGTC TACCTGGATG TCCAAGAGAA ATGGGGCTTG
 1261 GAGGACGTCA TGTTGATGGG CGACTTCAAT GCGGGCTGCA GCTATGTGAG ACCCTCCAG
 1321 TGGTCATCCA TCCGCCTGTG GACAAGCCCC ACCTTCCAGT GGCTGATCCC CGACAGCGCT
 1381 GACACCACAG CTACACCCAC GCACTGTGCC TATGACAGGA TCGTGGTTGC AGGGATGCTG
 1441 CTCCGAGGGG CCGTTGTTCC CGACTCGGCT CTTCCTTTA ACTTCCAGGC TGCCTATGGC
 1501 CTGAGTGACC AACTGGCCCA AGCCATCAGT GACCACTATC CAGTGGAGGT GATGCTGAAG
 1561 GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT TGA

//

Fig. 6(C)

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

 M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

 S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

 V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

 W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

 G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

 R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

 D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

 W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

 V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

 G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

 G A L T S G V H T F P A V L Q S S G

Fig. 6(D)
 (Sheet 1 of 3)

		603				612				621				630				639				648	
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q						
		657				666				675				684				693				702	
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K						
		711				720				729				738				747				756	
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P						
		765				774				783				792				801				810	
GAA	GGG	AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
E	G	S	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E						
		819				828				837				846				855				864	
ACC	AAG	ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
T	K	M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R						
		873				882				891				900				909				918	
TAC	GAC	ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
Y	D	I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G						
		927				936				945				954				963				972	
AAG	CTG	CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
K	L	L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V						
		981				990				999				1008				1017				1026	
AGT	GAG	CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
S	E	P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R						
		1035				1044				1053				1062				1071				1080	
CCT	GAC	CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
P	D	Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P						
		1089				1098				1107				1116				1125				1134	
TGC	GGG	AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTG	AGG	TTC	TTC	TCC	CGG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
C	G	N	D	T	F	N	R	E	P	A	I												

Fig. 6D
(Sheet 3 of 3)

pAS34

LOCUS PAS34.DNA 2196 bp 2196 bp 2196 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 34
 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file)
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS79 and AS80
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 501 a 677 c 607 g 411 t
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAActCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAGG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACTA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTTC TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CTTGCGGGAA CGACACCTTC
1741 AACCAGAGAG CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCTCC CAGTGGTCAT CCATCCGCTT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCAGACAG GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCCGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAACCTCCA GGCTGCCTAT GGCCTGAGTG ACCAACTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGTGA

```

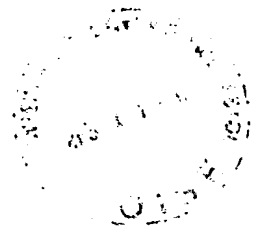
//

Fig. 7(A)

	9				18				27				36				45				54			
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H						
	63				72				81				90				99				108			
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	<u>S</u>	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S						
	117				126				135				144				153				162			
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E						
	171				180				189				198				207				216			
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P						
	225				234				243				252				261				270			
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T						
	279				288				297				306				315				324			
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E						
	333				342				351				360				369				378			
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y						
	387				396				405				414				423				432			
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S						
	441				450				459				468				477				486			
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L						
	495				504				513				522				531				540			
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA						
	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S						
	549				558				567				576				585				594			

Year	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

- 3 -



2061				2070				2079				2088				2097				2106	
ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC	GAC	TCG	GCT	CTT				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
I	V	V	A	G	M	L	L	R	G	A	V	V	P	D	S	A	L				
2115				2124				2133				2142				2151				2160	
CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG	GCC	CAA	GCC	ATC				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---		
P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L	A	Q	A	I				
2169				2178				2187				2196									
AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'									
---	---	---	---	---	---	---	---	---	---	---	---	---									
S	D	H	Y	P	V	E	V	M	L	K	*										

Fig. 7(B)
(Sheet 4 of 4)

pAS35

LOCUS PAS35.DNA 2193 bp 2193 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 35
 DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS81 and AS82
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
 SITES Note
 BASE COUNT 500 a 677 c 606 g 410 t
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAActCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCAAC
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCTAGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAAGGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGAAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGGTTACAG AGGTCAGGGA GTTTGCCATT
1801 GTTCCCCTGC ATGCGGCCCC GGGGGACGCA GTAGCCGAGA TCGACGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCAG TGGTCATCCA TCCGCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGGAGGT GATGCTGAAG TGA
  
```

//

Fig. 8(A)

5'		9		18		27		36		45		54						
	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
		63		72		81		90		99		108						
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
		117		126		135		144		153		162						
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
		171		180		189		198		207		216						
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
		225		234		243		252		261		270						
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
		279		288		297		306		315		324						
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
		333		342		351		360		369		378						
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
		387		396		405		414		423		432						
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
		441		450		459		468		477		486						
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
		495		504		513		522		531		540						
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
		549		558		567		576		585		594						
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G
		603		612		621		630		639		648						
	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG
	L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q
		657		666		675		684		693		702						

Fig. 8(B)
(Sheet 1 of 4)

Fig. 8(B)
(Sheet 3 of 4)

2061	2070	2079	2088	2097	2106
GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC					
-----	-----	-----	-----	-----	-----
V V A G M L L R G A V V P D S A L P					
2115	2124	2133	2142	2151	2160
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT					
-----	-----	-----	-----	-----	-----
F N F Q A A Y G L S D Q L A Q A I S					
2169	2178	2187			
GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'					
-----	-----	-----	-----	-----	-----
D H Y P V E V M L K *					

Fig. 8(B)
(Sheet 4 of 4)

pAS36

LOCUS PAS36.DNA 2190 bp 2190 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 36
 DEFINITION Clone 18.24.1 with residue 1392 T > C
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS83 and AS84
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 FEATURES Residue 1392 T > C silent S to S mutation
 SITES Note
 BASE COUNT 498 a 678 c 605 g 409 t
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCG CAAATCTTGT
721 GACAAAAC TCACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCC AAAACC CAAGGACACC CTCATGATCT CCGGACCCC TGAGGTCACA
841 TGCCTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGGAG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGA CTG CCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGT CAGGTT CTTCTCCCGG TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGGCCCCGGG GGACGCAGTA GCCGAGATCG ACGCTCTCTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGTGA
  
```

//

Fig. 9(A)

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC GAC

M G W S C I I L F L V A T A T G V H

TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

S Q V Q L V Q S G A E V K K P G A S

GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

V K V S C K A S G Y T F S A Y W I E

TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

W V R Q A P G K G L E W V G E I L P

GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

G S N N S R Y N E K F K G R V T V T

AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

R D T S T N T A Y M E L S S L R S E

GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

D T A V Y Y C A R S Y D F A W F A Y

TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

W G Q G T L V T V S S A S T K G P S

GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

V F P L A P S S K S T S G G T A A L

GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

G C L V K D Y F P E P V T V S W N S

GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

G A L T S G V H T F P A V L Q S S G

CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG

L Y S L S S V V T V P S S S L G T Q

657 666 675 684 693 702

Fig. 9(B)
(Sheet 1 of 4)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA
 T Y I C N V N H K P S N T K V D K K

711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT
 V E P K S C D K T H T C P P C P A P

765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC
 E L L G G P S V F L F P P K P K D T

819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC
 L M I S R T P E V T C V V V D V S H

873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT
 E D P E V K F N W Y V D G V E V H N

927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC
 A K T K P R E E Q Y N S T Y R V V S

981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG
 V L T V L H Q D W L N G K E Y K C K

1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA
 V S N K A L P A P I E K T I S K A K

1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG
 G Q P R E P Q V Y T L P P S R D E L

1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC
 T K N Q V S L T C L V K G F Y P S D

1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG
 I A V E W E S N G Q P E N N Y K T T

1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG
 P P V L D S D G S F F L Y S K L T V

1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG
 D K S R W Q Q G N V F S C S V M H E

Fig. 9(B)
(Sheet 2 of 4)

GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCC	CCG	GGG	AGC	GGC
A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	<u>G</u>	<u>S</u>	<u>G</u>
1413	1422	1431	1440	1449	1458												
GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG	ATG	TCC
<u>G</u>	<u>L</u>	<u>K</u>	<u>I</u>	<u>A</u>	<u>A</u>	<u>F</u>	<u>N</u>	<u>I</u>	<u>Q</u>	<u>T</u>	<u>F</u>	<u>G</u>	<u>E</u>	<u>T</u>	<u>K</u>	<u>M</u>	<u>S</u>
1467	1476	1485	1494	1503	1512												
AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC	ATC	GCC
N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D	I	A
1521	1530	1539	1548	1557	1566												
CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG	CTG	GAC
L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L	L	D
1575	1584	1593	1602	1611	1620												
AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG	CCA	CTG
N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E	P	L
1629	1638	1647	1656	1665	1674												
GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC	CAG	GTG
G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D	Q	V
1683	1692	1701	1710	1719	1728												
TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG	AAC	GAC
S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G	N	D
1737	1746	1755	1764	1773	1782												
ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTG	AGG	TTC	TTC	TCC	CGG	TTC	ACA	GAG	GTC
T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T	E	V
1791	1800	1809	1818	1827	1836												
AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA	GCC	GAG
R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V	A	E
1845	1854	1863	1872	1881	1890												
ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA	GAG	AAA	TGG	GGC	TTG	GAG
I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G	L	E
1899	1908	1917	1926	1935	1944												
GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA	CCC	TCC
D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R	P	S
1953	1962	1971	1980	1989	1998												
CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG	ATC	CCC
Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L	I	P
2007	2016	2025	2034	2043	2052												
GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG	ATC	GTG
D	S	A	D	T	T	A	T	P	T	H	C	A	Y	D	R	I	V

Fig. 9(B)
(Sheet 3 of 4)

2061 2070 2079 2088 2097 2106

2061	2070	2079	2088	2097	2106
GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC TTT					
-----	-----	-----	-----	-----	-----
V A G M L L R G A V V P D S A L P F					
2115	2124	2133	2142	2151	2160
AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT GAC					
-----	-----	-----	-----	-----	-----
N F Q A A Y G L S D Q L A Q A I S D					
2169	2178	2187			
CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'					
-----	-----	-----			
H Y P V E V M L K *					

Fig. 9(B)
(Sheet 4 of 4)

pAS37

LOCUS PAS37.DNA 2226 bp 2196 bp 2196 bp DNA 14-AUG-1998
 DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 37
 DEFINITION Clone 16.4.2 (same as hcdnasel.dna template file) plus NLS
 REFERENCE
 AUTHORS VERHOEYEN ET AL
 TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
 JOURNAL IMMUNOL. (1993):78, 364-370
 COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
 COMMENT The fusion was made using overlapping oligos AS79 and AS80
 FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
 FEATURES Residue 963 is G > T leading to silent mutation in all clones
 SITES Note
 BASE COUNT 511 a 683 c 619 g 413 t
 ORIGIN ?

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTGCGCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAGTCA
541 GCGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCA GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGGGTAA AGGGAGCGC GGGCTGAAGA TCGCAGCCTT CAACATCCAG
1441 ACATTTGGGG AGACCAAGAT GTCCAATGCC ACCCTCGTCA GCTACATTGT GCAGATCCTG
1501 AGCCGCTACG ACATCGCCCT GGTCCAGGAG GTCAGAGACA GCCACCTGAC TGCCGTGGGG
1561 AAGCTGCTGG ACAACCTCAA TCAGGACGCA CCAGACACCT ATCACTACGT GGTCACTGAG
1621 CCACTGGGAC GGAACAGCTA TAAGGAGCGC TACCTGTTCTG TGTACAGGCC TGACCAGGTG
1681 TCTGCGGTGG ACAGCTACTA CTACGATGAT GGCTGCGAGC CCTGCGGGAA CGACACCTTC
1741 AACCAGAGAG CAGCCATTGT CAGGTTCTTC TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC
1801 ATTGTTCCCC TGCATGCGGC CCCGGGGGAC GCAGTAGCCG AGATCGACGC TCTCTATGAC
1861 GTCTACCTGG ATGTCCAAGA GAAATGGGGC TTGGAGGACG TCATGTTGAT GGGCGACTTC
1921 AATGCGGGCT GCAGCTATGT GAGACCTCC CAGTGGTCAT CCATCCGCTT GTGGACAAGC
1981 CCCACCTTCC AGTGGCTGAT CCCCACAGC GCTGACACCA CAGCTACACC CACGCACTGT
2041 GCCTATGACA GGATCGTGGT TGCAGGGATG CTGCTCCGAG GGGCGGTTGT TCCCGACTCG
2101 GCTCTTCCCT TTAACCTCCA GGCTGCCTAT ACCAAGTGGC CCAAGCCATC
2161 AGTGACCACT ATCCAGTGGA GGTGATGCTG AAGGGGGGCG GACCCAAAA GAAGCGCAAG
2221 GTTTGA

```

//

NLS

Fig. 10(A)

	9					18			27			36			45			54		
5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC																				
M G W S C I I L F L V A T A T G V H																				
TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA	63					72			81			90			99			108		
S Q V Q L V Q S G A E V K K P G A S																				
GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG	117					126			135			144			153			162		
V K V S C K A S G Y T F S A Y W I E																				
TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT	171					180			189			198			207			216		
W V R Q A P G K G L E W V G E I L P																				
GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT	225					234			243			252			261			270		
G S N N S R Y N E K F K G R V T V T																				
AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG	279					288			297			306			315			324		
R D T S T N T A Y M E L S S L R S E																				
GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC	333					342			351			360			369			378		
D T A V Y Y C A R S Y D F A W F A Y																				
TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG	387					396			405			414			423			432		
W G Q G T L V T V S S A S T K G P S																				
GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG	441					450			459			468			477			486		
V F P L A P S S K S T S G G T A A A L																				
GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG AC G TG TCG TGG AAC TCA	495					504			513			522			531			540		
G C L V K D Y F P E P V T V S W N S																				
GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA	549					558			567			576			585			594		
G A L T S G V H T F P A V L Q S S G																				
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG	603					612			621			630			639			648		
L Y S L S S V V T V P S S S L G T Q																				
	657					666			675			684			693			702		

Fig. 10(B)
(Sheet 1 of 4)

1359				1368			1377				1386			1395			1404		
GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	GGT	AAA	GGG		

A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	G	K	<u>G</u>		

1413				1422			1431				1440			1449			1458		
AGC	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG		

<u>S</u>			<u>G</u>	<u>G</u>	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K

1467				1476			1485				1494			1503			1512		
ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC		

M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D		

1521				1530			1539				1548			1557			1566		
ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG		

I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L		

1575				1584			1593				1602			1611			1620		
CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG		

L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E		

1629				1638			1647				1656			1665			1674		
CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC		

P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D		

1683				1692			1701				1710			1719			1728		
CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG		

Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G		

1737				1746			1755				1764			1773			1782		
AAC	GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTG	AGG	TTC	TTC	TCC	CGG	TTC	ACA		

N	D	T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T		

1791				1800			1809				1818			1827			1836		
GAG	GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA		

E	V	R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V		

1845				1854			1863				1872			1881			1890		
GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTG	TAC	CTG	GAT	GTG	CAA	GAG	AAA	TGG	GGC		

A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G		

1899				1908			1917				1926			1935			1944		
TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA		

L	E	D	V	M	L	M	G	D	F	N	A	G	C	S	Y	V	R		

1953				1962			1971				1980			1989			1998		
CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC	TTC	CAG	TGG	CTG		

P	S	Q	W	S	S	I	R	L	W	T	S	P	T	F	Q	W	L		

2067				2016			2025				2034			2043			2052		
ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT	GCC	TAT	GAC	AGG		

I	P	D	S	A	D	T	T	A											

Fig. 10(B)
(Sheet 4 of 4)

pAS38

LOCUS PAS38.DNA 2223 bp 2193 bp DNA 14-AUG-1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase construct 38
DEFINITION Clone 17.12.1 with silent K to K mutation (1398 A > G)+NLS
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS81 and AS82
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES In 17.12.1 residue 1398 is A > G (silent K to K mutation)
SITES Note
BASE COUNT 510 a 683 c 618 g 412 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CTTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCCA CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTTCTCTTCC CCCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCCTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCCTCCCGT CTGGACTCC
1261 GACGGCTCCT TCTTCCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CTCCGAAgGG GAGCGGCGGG CTGAAGATCG CAGCCTTCAA CATCCAGACA
1441 TTTGGGGAGA CCAAGATGTC CAATGCCACC CTCGTCAGCT ACATTGTGCA GATCCTGAGC
1501 CGCTACGACA TCGCCCTGGT CCAGGAGGTC AGAGACAGCC ACCTGACTGC CGTGGGGGAG
1561 CTGCTGGACA ACCTCAATCA GGACGCACCA GACACCTATC ACTACGTGGT CAGTGAGCCA
1621 CTGGGACGGA ACAGCTATAA GGAGCGCTAC CTGTTCTGTG ACAGGCCTGA CCAGGTGTCT
1681 GCGGTGGACA GCTACTACTA CGATGATGGC TGCGAGCCCT GCGGGAACGA CACCTTCAAC
1741 CGAGAGCCAG CCATTGTCAG GTTCTTCTCC CGTTTCACAG AGGTACAGGA GTTTGCCATT
1801 GTTCCCCTGC ATGCGGCCCC GGGGACGCA GTAGCCGAGA TCGAGCTCT CTATGACGTC
1861 TACCTGGATG TCCAAGAGAA ATGGGGCTTG GAGGACGTCA TGTTGATGGG CGACTTCAAT
1921 GCGGGCTGCA GCTATGTGAG ACCCTCCCAG TGGTCATCCA TCCGCCTGTG GACAAGCCCC
1981 ACCTTCCAGT GGCTGATCCC CGACAGCGCT GACACCACAG CTACACCCAC GCACTGTGCC
2041 TATGACAGGA TCGTGGTTGC AGGGATGCTG CTCCGAGGGG CCGTTGTTCC CGACTCGGCT
2101 CTTCCCTTTA ACTTCCAGGC TGCCTATGGC CTGAGTGACC AACTGGCCCA AGCCATCAGT
2161 GACCACTATC CAGTGAGGAT GATGCTGAAG GGGGGCGGAC CCAAAAAGAA GCGCAAGGTT
2221 TGA

//

—NLS

Fig. 11(A)

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA

 T Y I C N V N H K P S N T K V D K K

711 720 729 738 747 756
 GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC CCA CCG TGC CCA GCA CCT

 V E P K S C D K T H T C P P C P A P

765 774 783 792 801 810
 GAA CTC CTG GGG GGA CCG TCA GTC TTC CTC TTC CCC CCA AAA CCC AAG GAC ACC

 E L L G G P S V F L F P P K P K D T

819 828 837 846 855 864
 CTC ATG ATC TCC CGG ACC CCT GAG GTC ACA TGC GTG GTG GTG GAC GTG AGC CAC

 L M I S R T P E V T C V V V D V S H

873 882 891 900 909 918
 GAA GAC CCT GAG GTC AAG TTC AAC TGG TAC GTG GAC GGC GTG GAG GTG CAT AAT

 E D P E V K F N W Y V D G V E V H N

927 936 945 954 963 972
 GCC AAG ACA AAG CCG CGG GAG GAG CAG TAC AAC AGC ACG TAC CGT GTG GTC AGC

 A K T K P R E E Q Y N S T Y R V V S

981 990 999 1008 1017 1026
 GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAT GGC AAG GAG TAC AAG TGC AAG

 V L T V L H Q D W L N G K E Y K C K

1035 1044 1053 1062 1071 1080
 GTC TCC AAC AAA GCC CTC CCA GCC CCC ATC GAG AAA ACC ATC TCC AAA GCC AAA

 V S N K A L P A P I E K T I S K A K

1089 1098 1107 1116 1125 1134
 GGG CAG CCC CGA GAA CCA CAG GTG TAC ACC CTG CCC CCA TCC CGG GAT GAG CTG

 G Q P R E P Q V Y T L P P S R D E L

1143 1152 1161 1170 1179 1188
 ACC AAG AAC CAG GTC AGC CTG ACC TGC CTG GTC AAA GGC TTC TAT CCC AGC GAC

 T K N Q V S L T C L V K G F Y P S D

1197 1206 1215 1224 1233 1242
 ATC GCC GTG GAG TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG

 I A V E W E S N G Q P E N N Y K T T

1251 1260 1269 1278 1287 1296
 CCT CCC GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AAG CTC ACC GTG

 P P V L D S D G S F F L Y S K L T V

1305 1314 1323 1332 1341 1350
 GAC AAG AGC AGG TGG CAG CAG GGG AAC GTC TTC TCA TGC TCC GTG ATG CAT GAG

 D K S R W Q Q G N V F S C S V H H E

Fig. 11(B)
(Sheet 2 of 4)

	1359				1368			1377			1386			1395			1404	
GCT	CTG	CAC	AAC	CAC	TAC	ACG	CAG	AAG	AGC	CTC	TCC	CTG	TCT	CCG	AAG	GGG	AGC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
A	L	H	N	H	Y	T	Q	K	S	L	S	L	S	P	K	<u>G</u>	<u>S</u>	
	1413				1422			1431			1440			1449			1458	
GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG	ATG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
<u>G</u>	<u>G</u>	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K	M	
	1467				1476			1485			1494			1503			1512	
TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC	ATC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D	I	
	1521				1530			1539			1548			1557			1566	
GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG	CTG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L	L	
	1575				1584			1593			1602			1611			1620	
GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG	CCA	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E	P	
	1629				1638			1647			1656			1665			1674	
CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTC	GTG	TAC	AGG	CCT	GAC	CAG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D	Q	
	1683				1692			1701			1710			1719			1728	
GTG	TCT	CGC	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG	AAC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G	N	
	1737				1746			1755			1764			1773			1782	
GAC	ACC	TTC	AAC	CGA	GAG	CCA	GCC	ATT	GTC	AGG	TTC	TTC	TCC	CGG	TTC	ACA	GAG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
D	T	F	N	R	E	P	A	I	V	R	F	F	S	R	F	T	E	
	1791				1800			1809			1818			1827			1836	
GTC	AGG	GAG	TTT	GCC	ATT	GTT	CCC	CTG	CAT	GCG	GCC	CCG	GGG	GAC	GCA	GTA	GCC	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
V	R	E	F	A	I	V	P	L	H	A	A	P	G	D	A	V	A	
	1845				1854			1863			1872			1881			1890	
GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA	GAG	AAA	TGG	GGC	TTG	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
E	I	D	A	L	Y	D	V	Y	L	D	V	Q	E	K	W	G	L	
	1899				1908			1917			1926			1935			1944	
GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC	AGC	TAT	GTG	AGA	CCC	

Fig. 11(C)
(Sheet 3 of 4)

019

2061	2070	2079	2088	2097	2106
GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT CCC					
-----	-----	-----	-----	-----	-----
V V A G M L L R G A V V P D S A L P					
2115	2124	2133	2142	2151	2160
TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC AGT					
-----	-----	-----	-----	-----	-----
F N F Q A A Y G L S D Q L A Q A I S					
2169	2178	2187	2196	2205	2214
GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG CGC					
-----	-----	-----	-----	-----	-----
D H Y P V E V M L K			<u>G G G P K K K R</u>		
2223					
AAG GTT TGA 3'					

K V *					
=====					

Fig. 11(D)
(Sheet 4 of 4)

pAS39

LOCUS PAS39.DNA 2220 bp 2190 bp DNA
1998
DEFINITION HUMANISED HMFG1 heavy chain fused to human DNase - construct 39
DEFINITION Clone 18.24.1 with residue 1392 T > C +NLS
REFERENCE
AUTHORS VERHOEYEN ET AL
TITLE CONSTRUCTION OF RESHAPED HMFG1 etc
JOURNAL IMMUNOL. (1993):78, 364-370
COMMENT Human DNase sequence is modified as a result of oligo assembly (mhdnase.dna)
COMMENT The fusion was made using overlapping oligos AS83 and AS84
FEATURES AA RESIDUE 235 HAS NOT BEEN CHANGED TO KABAT (I.E. V TO A)
FEATURES Residue 963 is G > T leading to silent mutation in all clones
FEATURES Residue 1392 T > C silent S to S mutation
SITES Note
BASE COUNT 508 a 684 c 617 g 411 t
ORIGIN ?

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATAACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTIONTTC CCCGAACCGG TGACGGTGTC GTGGAACCTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAC TCCTGGGGGG ACCGTCAGTC
781 TTCCTCTTCC CCCCAAAACC CAAGGACACC CTCATGATCT CCCGGACCCC TGAGGTCACA
841 TGCGTGGTGG TGGACGTGAG CCACGAAGAC CCTGAGGTCA AGTTCAACTG GTACGTGGAC
901 GGCGTGGAGG TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTACAA CAGCACGTAC
961 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAATGGCAA GGAGTACAAG
1021 TGCAAGGTCT CCAACAAAGC CCTCCCAGCC CCCATCGAGA AAACCATCTC CAAAGCCAAA
1081 GGGCAGCCCC GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
1141 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT CGCCGTGGAG
1201 TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA CGCTCCCGT GCTGGACTCC
1261 GACGGCTCCT TCTTCTCTA CAGCAAGCTC ACCGTGGACA AGAGCAGGTG GCAGCAGGGG
1321 AACGTCTTCT CATGCTCCGT GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC
1381 CTCTCCCTGT CcCCGGGGAG CGGCGGGCTG AAGATCGCAG CCTTCAACAT CCAGACATTT
1441 GGGGAGACCA AGATGTCCAA TGCCACCCTC GTCAGCTACA TTGTGCAGAT CCTGAGCCGC
1501 TACGACATCG CCCTGGTCCA GGAGGTCAGA GACAGCCACC TGACTGCCGT GGGGAAGCTG
1561 CTGGACAACC TCAATCAGGA CGCACCAGAC ACCTATCACT ACGTGGTCAG TGAGCCACTG
1621 GGACGGAACA GCTATAAGGA GCGCTACCTG TTCGTGTACA GGCCTGACCA GGTGTCTGCG
1681 GTGGACAGCT ACTACTACGA TGATGGCTGC GAGCCCTGCG GGAACGACAC CTTCAACCGA
1741 GAGCCAGCCA TTGTCAGGTT CTTCTCCCGT TTCACAGAGG TCAGGGAGTT TGCCATTGTT
1801 CCCCTGCATG CGCCCCGGG GACGCGAGTA GCCGAGATCG ACGTCTCTTA TGACGTCTAC
1861 CTGGATGTCC AAGAGAAATG GGGCTTGGAG GACGTCATGT TGATGGGCGA CTTCAATGCG
1921 GGCTGCAGCT ATGTGAGACC CTCCAGTGG TCATCCATCC GCCTGTGGAC AAGCCCCACC
1981 TTCCAGTGGC TGATCCCCGA CAGCGCTGAC ACCACAGCTA CACCCACGCA CTGTGCCTAT
2041 GACAGGATCG TGGTTGCAGG GATGCTGCTC CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT
2101 CCCTTTAACT TCCAGGCTGC CTATGGCCTG AGTGACCAAC TGGCCCAAGC CATCAGTGAC
2161 CACTATCCAG TGGAGGTGAT GCTGAAGGGG GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

//

Fig. 12(A)

	9				18				27				36				45				54	
5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC				
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H				
	63				72				81				90				99				108	
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA				
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S				
	117				126				135				144				153				162	
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG				
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E				
	171				180				189				198				207				216	
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT				
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P				
	225				234				243				252				261				270	
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT				
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T				
	279				288				297				306				315				324	
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG				
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E				
	333				342				351				360				369				378	
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC				
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y				
	387				396				405				414				423				432	
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG				
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S				
	441				450				459				468				477				486	
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG				
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L				
	495				504				513				522				531				540	
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA				
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S				
	549				558				567				576				585				594	
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA				
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G				
	603				612				621				630				639				648	
	CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG				
	L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q				
	657				666				675				684				693				702	

Fig. 12(B)
(Sheet 1 of 4)

Fig. 12(B)
(Sheet 2 of 4)

GCT CTG CAC AAC CAC TAC ACG CAG AAG AGC CTC TCC CTG TCC CCG GGG AGC GGC
 A L H N H Y T Q K S L S L S P G S G

1413 1422 1431 1440 1449 1458
 GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT GGG GAG ACC AAG ATG TCC
G L K I A A F N I Q T F G E T K M S

1467 1476 1485 1494 1503 1512
 AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG AGC CGC TAC GAC ATC GCC
 N A T L V S Y I V Q I L S R Y D I A

1521 1530 1539 1548 1557 1566
 CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC GTG GGG AAG CTG CTG GAC
 L V Q E V R D S H L T A V G K L L D

1575 1584 1593 1602 1611 1620
 AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC GTG GTC AGT GAG CCA CTG
 N L N Q D A P D T Y H Y V V S E P L

1629 1638 1647 1656 1665 1674
 GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG TAC AGG CCT GAC CAG GTG
 G R N S Y K E R Y L F V Y R P D Q V

1683 1692 1701 1710 1719 1728
 TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC GAG CCC TGC GGG AAC GAC
 S A V D S Y Y Y D D G C E P C G N D

1737 1746 1755 1764 1773 1782
 ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC TCC CGG TTC ACA GAG GTC
 T F N R E P A I V R F F S R F T E V

1791 1800 1809 1818 1827 1836
 AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG GGG GAC GCA GTA GCC GAG
 R E F A I V P L H A A P G D A V A E

1845 1854 1863 1872 1881 1890
 ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC TTG GAG
 I D A L Y D V Y L D V Q E K W G L E

1899 1908 1917 1926 1935 1944
 GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA CCC TCC
 D V M L M G D F N A G C S Y V R P S

1953 1962 1971 1980 1989 1998
 CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG ATC CCC
 Q W S S I R L W T S P T F Q W L I P

2007 2016 2025 2034 2043 2052
 GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG ATC GTG
 D S A D T T A T P T H C A Y D R I V

Fig. 12(B)
(Sheet 3 of 4)

GTT TGA 3'

V *

Fig. 12(B)
(Sheet 4 of 4)

pAS101

LOCUS PAS101.DNA 1548 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS101)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic
 fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 343 a 467 c 430 g 308 t
 ORIGIN

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAGTCA
541 GCGGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCCC ACCGTGCCCA GCACCTGAAG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCTT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA CCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

```

//

Fig. 13(A)

LOCUS FDDNASE101 1548 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag join(1..>720,<781..1548)

frag 721..780

frag join(721..>735,<736..>759,<760..>780)

BASE COUNT 343 A 465 C 431 G 309 T 0 OTHER

ORIGIN -

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC

121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA

181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT

241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG

301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC

361 TTTGCCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC

421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG

481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAActCA

541 GGC GCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC

601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC

661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT

721 GACAAAATC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC

781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT

841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG

901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC

961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG

1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG

1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC

1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCGGGGG ACGCAGTAGC CGAGATCGAC

1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGAGGA CGTCATGTTG

1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC

1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA

1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAAGGA TGCTGCTCCG AGGGGCCGTT

1441 GTTCCCAGCT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG

1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGTGA

//

Fig. 13(B)

30

LOCUS FDDNASE101 1557 BP SS-DNA SYN 29-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag 10..1557

/note="1 to 1548 of FdDNase101correct"

frag join(10..>729,<790..1557)

/note="1 to 1548 of PAS101.dna [Split]"

frag 730..789

/note="1 to 60 of 101/105linker"

frag join(730..>744,<745..>768,<769..>789)

/note="1 to 80 of 102linker [Split]"

BASE COUNT 344 A 471 C 433 G 309 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC

61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG

121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC

181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT

241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA

301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA

361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA

421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG

481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG

541 TGGAATCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA

601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC

661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC

721 AAATCTTGTG ACAAACCTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG

781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCTCGTC

841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC

901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACTCA ATCAGGACGC ACCAGACACC

961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTT

1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG

1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTT

1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCCAGGGGA CGCAGTAGCC

1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTTGGAGGAC

1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCCTC CCAGTGGTCA

1321 TCCATCCGCC TGTGGACAAG CCCCACCTTC CAGTGGCTGA TCCCCGACAG CGCTGACACC

1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA

1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTAACTTCC AGGCTGCCTA TGGCCTGAGT

1501 GACCAACTGG CCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGTGA

//

Fig. 13(C)

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

 M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

 S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

 V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

 W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

 G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

 R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

 D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

 W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

 V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

 G C L V K D Y F P E P V T V S W N S

549 558 567 576 585 594
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

 G A L T S G V H T F P A V L Q S S G

Fig. 13(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC	CTC AGC AGC GTG GTG	ACC GTG CCC	TCC AGC AGC TTG	GGC ACC	CAG
L Y S	L S S V V	T V P	S S S L	G T	Q
657	666	675	684	693	702
ACC TAC ATC	TGC AAC GTG AAT CAC	AAG CCC AGC AAC	ACC AAG GTG	GAC AAG	AAA
T Y I	C N V N H	K P S	N T K	V D K	K
711	720	729	738	747	756
GTT GAG CCC	AAA TCT TGT GAC	AAA ACT CAC	ACA TGC CCA	CCG TGC CCA	GCA CCT
V E P	K S C D K	T H T	C P P	C P A	P
765	774	783	792	801	810
GAA GGC GGG	CTG AAG ATC GCA	GCC TTC AAC	ATC CAG ACA	TTT GGG	GAG ACC AAG
E G G	L K I A A	F N I Q	T F G	E T K	
819	828	837	846	855	864
ATG TCC AAT	GCC ACC CTC GTC	AGC TAC ATT	GTG CAG ATC	CTG AGC CGC	TAC GAC
M S N	A T L V S	Y I V Q	I L S R	Y D	
873	882	891	900	909	918
ATC GCC CTG	GTC CAG GAG GTC	AGA GAC AGC	CAC CTG ACT	GCC GTG GGG	AAG CTG
I A L	V Q E V R	D S H L	T A V G	K L	
927	936	945	954	963	972
CTG GAC AAC	CTC AAT CAG GAC	GCA CCA GAC	ACC TAT CAC	TAC GTG GTC	AGT GAG
L D N	L N Q D A	P D T Y	H Y V V	S E	
981	990	999	1008	1017	1026
CCA CTG GGA	CGG AAC AGC TAT	AAG GAG CGC	TAC CTG TTC	GTG TAC AGG	CCT GAC
P L G	R N S Y K	E R Y L	F V Y R	P D	
1035	1044	1053	1062	1071	1080
CAG GTG TCT	GCG GTG GAC AGC	TAC TAC TAC	GAT GAT GGC	TGC GAG CCC	TGC GGG
Q V S	A V D S Y	Y Y Y D	D G C E	P C G	
1089	1098	1107	1116	1125	1134
AAC GAC ACC	TTC AAC CGA GAG	CCA GCC ATT	GTC AGG TTC	TTC TCC CGG	TTC ACA
N D T	F N R E P	A I V R	F F S R	F T	
1143	1152	1161	1170	1179	1188
GAG GTC AGG	GAG TTT GCC	ATT GTT CCC	CTG CAT GCG	GCC CCG GGG	GAC GCA GTA
E V R	E F A I V	P L H A	A P G D	A V	
1197	1206	1215	1224	1233	1242

Fig. 13(D)
(Sheet 2 of 3)



GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC

A E I D A L Y D V Y L D V Q E K W G

1251 1260 1269 1278 1287 1296
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA

L E D V M L M G D F N A G C S Y V R

1305 1314 1323 1332 1341 1350
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG

P S Q W S S I R L W T S P T F Q W L

1359 1368 1377 1386 1395 1404
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG

I P D S A D T T A T P T H C A Y D R

1413 1422 1431 1440 1449 1458
ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT

I V V A G M L L R G A V V P D S A L

1467 1476 1485 1494 1503 1512
CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC

P F N F Q A A Y G L S D Q L A Q A I

1521 1530 1539 1548
AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

S D H Y P V E V M L K *

Fig. 13(D)
(Sheet 3 of 3)

pAS102

LOCUS PAS102.DNA 1566 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS102)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna) (See Figure 2)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 345 a 469 c 440 g 312 t
ORIGIN

```
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTIONC CCCGAACCGG TGACGGTGTC GTGGAACCTA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTTG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTCTTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA
```

//

Fig. 14(A)



LOCUS FDDNASE102 1566 BP SS-DNA SYN 23-MAR-2001
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -
BASE COUNT 345 A 468 C 440 G 313 T 0 OTHER
ORIGIN -
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATT TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGA ACTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCACTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCAGACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAACCTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGTGA

//

Fig. 14(B)

pAS302

LOCUS FDDNASE302 1575 BP SS-DNA SYN 29-AUG-2000
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -

FEATURES Location/Qualifiers
frag 10..1575
/note="1 to 1566 of FdDNase102correct"

BASE COUNT 346 A 474 C 442 G 313 T 0 OTHER

ORIGIN -

1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCAGG GACGGTGTCTG
541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCCTCA
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTG TG ACAA AACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTTGGGGA GACCAAGATG
841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
1021 AAGGAGCGCT ACCTGTTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
1141 AGGTTCCTTCT CCCGGTTTCA AGAGGTCAGG GAGTTTGCCA TTGTTCCCCT GCATGCGGCC
1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
1321 AGACCCTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
1561 GTGATGCTGA AGTGA

//

Fig. 14(C)



GCC CCG GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT

A P G D A V A E I D A L Y D V Y L D

1251 1260 1269 1278 1287 1296
GTC CAA GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG

V Q E K W G L E D V M L M G D F N A

1305 1314 1323 1332 1341 1350
GGC TGC AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC

G C S Y V R P S Q W S S I R L W T S

1359 1368 1377 1386 1395 1404
CCC ACC TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG

P T F Q W L I P D S A D T T A T P T

1413 1422 1431 1440 1449 1458
CAC TGT GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT

H C A Y D R I V V A G M L L R G A V

1467 1476 1485 1494 1503 1512
GTT CCC GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC

V P D S A L P F N F Q A A Y G L S D

1521 1530 1539 1548 1557 1566
CAA CTG GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'

Q L A Q A I S D H Y P V E V M L K *

Fig. 14(D)
(Sheet 3 of 3)

pAS103

LOCUS PAS103.DNA 1560 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS103)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 344 a 468 c 436 g 312 t
ORIGIN

```
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAC TCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAAC TC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGA CTG CCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

//

Fig. 15(A)

15 AUG 2000

LOCUS FDDNASE103 1560 BP SS-DNA SYN 25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag join(1..>720,<793..1560)

frag 721..792

frag /note="1 to 72 of 103/107linker"

frag join(721..>771,<772..792)

frag /note="1 to 78 of 102linker [Split]"

BASE COUNT 344 A 467 C 436 G 313 T 0 OTHER

ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG

61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC

121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA

181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATAACAAT

241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG

301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC

361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC

421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG

481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA

541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC

601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC

661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT

721 GACAAACTC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG

781 AAGATCGCAG CTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC

841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA

901 GACAGCCACC TGACTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC

961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG

1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC

1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG

1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA

1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG

1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG

1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC

1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC

1441 CGAGGGGCCG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG

1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 15(B)

LOCUS FDDNASE103 1569 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -

FEATURES Location/Qualifiers
 frag 10..1569
 /note="1 to 1560 of FdDNase103correct"
 frag join(10..>729,<802..1569)
 /note="1 to 1560 of PAS103.dna [Split]"
 frag 730..801
 /note="1 to 72 of 103/107linker"
 frag join(730..>780,<781..801)
 /note="1 to 78 of 102linker [Split]"

BASE COUNT 345 A 473 C 438 G 313 T 0 OTHER
 ORIGIN -

```

1  GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
61  CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCTG
541 TGGAACCTAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCTCTCA
601 GGACTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTG TG ACAA AACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
781 GCGGGGCTGA AGATCGCAGC CTTCAACATC CAGACATT TG GGGAGACCAA GATGTCCAAT
841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAGCTGC TGGACAACCT CAATCAGGAC
961 GCACCAGACA CCTATCACTA CGTGGTCAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTC
1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
1261 GGCTTGGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
1381 AGCGCTGACA CCACAGCTAC ACCCACGCAC TGTGCCTATG ACAGGATCGT GGTTCAGGG
1441 ATGCTGCTCC GAGGGGCGGT TGTTCCTGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
1501 TATGGCCTGA GTGACCAACT GGCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
1561 CTGAAGTGA
  
```

//

Fig. 15(C)

5' ATG GGA TGG AGC TGT ATC ATC CTC TTC TTG GTA GCA ACA GCT ACA GGT GTC CAC

 M G W S C I I L F L V A T A T G V H

63 72 81 90 99 108
 TCC CAG GTG CAG CTG GTG CAG TCT GGG GCA GAG GTG AAA AAG CCT GGG GCC TCA

 S Q V Q L V Q S G A E V K K P G A S

117 126 135 144 153 162
 GTG AAG GTG TCC TGC AAG GCT TCT GGC TAC ACC TTC AGT GCC TAC TGG ATA GAG

 V K V S C K A S G Y T F S A Y W I E

171 180 189 198 207 216
 TGG GTG CGC CAG GCT CCA GGA AAG GGC CTC GAG TGG GTC GGA GAG ATT TTA CCT

 W V R Q A P G K G L E W V G E I L P

225 234 243 252 261 270
 GGA AGT AAT AAT TCT AGA TAC AAT GAG AAG TTC AAG GGC CGA GTG ACA GTC ACT

 G S N N S R Y N E K F K G R V T V T

279 288 297 306 315 324
 AGA GAC ACA TCC ACA AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGG TCT GAG

 R D T S T N T A Y M E L S S L R S E

333 342 351 360 369 378
 GAC ACA GCC GTC TAT TAC TGT GCA AGA TCC TAC GAC TTT GCC TGG TTT GCT TAC

 D T A V Y Y C A R S Y D F A W F A Y

387 396 405 414 423 432
 TGG GGC CAA GGG ACT CTG GTC ACA GTC TCC TCA GCC TCC ACC AAG GGC CCA TCG

 W G Q G T L V T V S S A S T K G P S

441 450 459 468 477 486
 GTC TTC CCC CTG GCA CCC TCC TCC AAG AGC ACC TCT GGG GGC ACA GCG GCC CTG

 V F P L A P S S K S T S G G T A A L

495 504 513 522 531 540
 GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG TCG TGG AAC TCA

 G C L V K D Y F P E P V T V S W N S

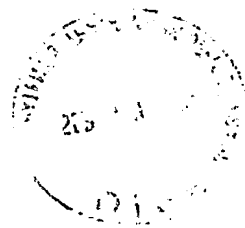
549 558 567 576 585 594
 GGC GCC CTG ACC AGC GGC GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC TCA GGA

 G A L T S G V H T F P A V L Q S S G

Fig. 15(D)
(Sheet 1 of 3)

648
CC CAG

T Q



```

GGG GAC GCA GTA GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA
---
G   D   A   V   A   E   I   D   A   L   Y   D   V   Y   L   D   V   Q

      1251      1260      1269      1278      1287      1296
GAG AAA TGG GGC TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC
---
E   K   W   G   L   E   D   V   M   L   M   G   D   F   N   A   G   C

      1305      1314      1323      1332      1341      1350
AGC TAT GTG AGA CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC
---
S   Y   V   R   P   S   Q   W   S   S   I   R   L   W   T   S   P   T

      1359      1368      1377      1386      1395      1404
TTC CAG TGG CTG ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT
---
F   Q   W   L   I   P   D   S   A   D   T   T   A   T   P   T   H   C

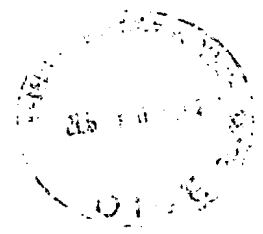
      1413      1422      1431      1440      1449      1458
GCC TAT GAC AGG ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC
---
A   Y   D   R   I   V   V   A   G   M   L   L   R   G   A   V   V   P

      1467      1476      1485      1494      1503      1512
GAC TCG GCT CTT CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG
---
D   S   A   L   P   F   N   F   Q   A   A   Y   G   L   S   D   Q   L

      1521      1530      1539      1548      1557
GCC CAA GCC ATC AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG TGA 3'
---
A   Q   A   I   S   D   H   Y   P   V   E   V   M   L   K   *

```

Fig. 15(D)
(Sheet 3 of 3)




pAS104

LOCUS PAS104.DNA 1560 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I (pAS104)
Position 924 G to A by ggg to gag
Linker GR instead of GG (position 777)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 346 a 468 c 434 g 312 t
ORIGIN

```
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAACCTA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCAGGCTG
781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTGAGA
901 GACAGCCACC TGA CTGCGGT GGAAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTGAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA
```

//

Fig. 16(A)


 25-AUG-2000

LOCUS FDDNASE104 1560 BP SS-DNA SYN
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -
 FEATURES Location/Qualifiers
 frag join(1..>720,<793..1560)
 /note="1 to 1560 of PAS104.dna [Split]"
 frag 721..792
 /note="1 to 72 of 104linker"
 frag join(721..>774,<776..792)
 /note="1 to 72 of 103linker [Split]"
 frag join(721..>771,<772..>774,<776..792)
 /note="1 to 78 of 102linker [Split]"
 BASE COUNT 346 A 467 C 434 G 313 T 0 OTHER
 ORIGIN -
 1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
 61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
 121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
 181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATAACAAT
 241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
 301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
 361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
 421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCAGACGG
 481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
 541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCTCTC AGGACTCTAC
 601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
 661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
 721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCAGGCTG
 781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
 841 GTCAGCTACA TTGTGCAGAT CTTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
 901 GACAGCCACC TGAAGTCCGT GGAGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
 961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
 1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
 1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAAGTT CTTCTCCCGG
 1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
 1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
 1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
 1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
 1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
 1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
 1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGTGA

//

Fig. 16(B)

603	612	621	630	639	648
CTC TAC TCC CTC AGC	AGC GTG GTG ACC	GTG CCC TCC AGC	AGC AGC TTG GGC	ACC CAG	
L Y S L S	S V V T V	P S S S	L G T	Q	
657	666	675	684	693	702
ACC TAC ATC TGC AAC	GTG AAT CAC AAG	CCC AGC AAC	ACC AAG GTG	GAC AAG	AAA
T Y I C N	V N H K P	S N T K	V D K	K	
711	720	729	738	747	756
GTT GAG CCC AAA TCT	TGT GAC AAA ACT	CAC ACA TGC	TGT GTG GAG	TGC CCA	CCG
V E P K S	C D K T	H T C C	V E C	P P	
765	774	783	792	801	810
TGC CCA GCA CCT GAA	GGC AGG CTG AAG	ATC GCA GCC	TTC AAC ATC	CAG ACA	TTT
C P A P E	G R L K I	A A F N	I Q T	F	
819	828	837	846	855	864
GGG GAG ACC AAG ATG	TCC AAT GCC ACC	CTC GTC AGC	TAC ATT GTG	CAG ATC	CTG
G E T K M	S N A T	L V S Y	I V Q I	L	
873	882	891	900	909	918
AGC CGC TAC GAC ATC	GCC CTG GTC CAG	GAG GTC AGA	GAC AGC CAC	CTG ACT	GCC
S R Y D I	A L V Q	E V R D	S H L T	A	
927	936	945	954	963	972
GTG GAG AAG CTG CTG	GAC AAC CTC AAT	CAG GAC GCA	CCA GAC ACC	TAT CAC	TAC
V E K L L	D N L N	Q D A P	D T Y H	Y	
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA	CTG GGA CGG AAC	AGC TAT AAG	GAG CGC TAC	CTG TTC	GTG
V V S E P	L G R N	S Y K E	R Y L F	V	
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG	GTG TCT GCG GTG	GAC AGC TAC	TAC TAC GAT	GAT GGC	TGC
Y R P D Q	V S A V	D S Y Y	Y D D	G C	
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC	GAC ACC TTC AAC	CGA GAG CCA	GCC ATT GTC	AGG TTC	TTC
E P C G N	D T F N	R E P A	I V R F	F	
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG	GTC AGG GAG TTT	GCC ATT GTT	CCC CTG CAT	GCG GCC	CCG
S R F T E	V R E F	A I V P	L H A A	P	
1197	1206	1215	1224	1233	1242

Fig. 16(C)
(Sheet 2 of 3)

GGG	GAC	GCA	GTA	GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT	GTC	CAA
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	D	A	V	A	E	I	D	A	L	Y	D	V	Y	L	D	V	Q
1251			1260			1269			1278			1287			1296		
GAG	AAA	TGG	GGC	TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG	GGC	TGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
E	K	W	G	L	E	D	V	M	L	M	G	D	F	N	A	G	C
1305			1314			1323			1332			1341			1350		
AGC	TAT	GTG	AGA	CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC	CCC	ACC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
S	Y	V	R	P	S	Q	W	S	S	I	R	L	W	T	S	P	T
1359			1368			1377			1386			1395			1404		
TTC	CAG	TGG	CTG	ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG	CAC	TGT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
F	Q	W	L	I	P	D	S	A	D	T	T	A	T	P	T	H	C
1413			1422			1431			1440			1449			1458		
GCC	TAT	GAC	AGG	ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT	GTT	CCC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A	Y	D	R	I	V	V	A	G	M	L	L	R	G	A	V	V	P
1467			1476			1485			1494			1503			1512		
GAC	TCG	GCT	CTT	CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC	CAA	CTG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
D	S	A	L	P	F	N	F	Q	A	A	Y	G	L	S	D	Q	L
1521			1530			1539			1548			1557					
GCC	CAA	GCC	ATC	AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	TGA	3'	
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
A	Q	A	I	S	D	H	Y	P	V	E	V	M	L	K	*		

Fig. 16(C)
(Sheet 3 of 3)

pAS105

LOCUS PAS105.DNA 1578 bp mRNA PRI 06-MAR-1995
 DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
 NLS (pAS105)
 ACCESSION
 NID
 KEYWORDS DNase I.
 SOURCE DNase I sequence is from assembled oligos (thus modified c/f
 MHDNASE1.dna)
 ORGANISM Homo sapiens
 Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
 Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Shak,S., Capon,D.J., Hellmiss,R., Marsters,S.A. and Baker,C.L.
 TITLE Recombinant human DNase I reduces the viscosity of cystic
 fibrosis
 sputum
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
 MEDLINE 91067672
 BASE COUNT 353 a 473 c 442 g 310 t
 ORIGIN

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCACTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAActCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGTGTCC TACAGTCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACTC ACACATGCCC ACCGTGCCCC GCACCTGAAG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCTCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCGGCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCCT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGCGTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
1561 AAGAAGCGCA AGGTTTGA

```

//

└─→ NLS

Fig. 17(A)

LOCUS FDDNASE105 1578 BP SS-DNA

SYN

25-AUG-2000

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

frag join(1..>720,<781..1578)
/note="1 to 1578 of PAS105.dna [Split]"

frag 721..780
/note="1 to 60 of 101/105linker"

frag join(721..>735,<736..>759,<760..>780)
/note="1 to 80 of 102linker [Split]"

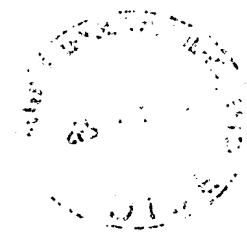
BASE COUNT 353 A 471 C 443 G 311 T 0 OTHER

ORIGIN -

```
1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAActCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAACTC ACACATGTCC ACCGTGTCCA GCACCAGAGG GCGGGCTGAA GATCGCAGCC
781 TTCAACATCC AGACATTTGG GGAGACCAAG ATGTCCAATG CCACCCTCGT CAGCTACATT
841 GTGCAGATCC TGAGCCGCTA CGACATCGCC CTGGTCCAGG AGGTCAGAGA CAGCCACCTG
901 ACTGCCGTGG GGAAGCTGCT GGACAACCTC AATCAGGACG CACCAGACAC CTATCACTAC
961 GTGGTCAGTG AGCCACTGGG ACGGAACAGC TATAAGGAGC GCTACCTGTT CGTGTACAGG
1021 CCTGACCAGG TGTCTGCGGT GGACAGCTAC TACTACGATG ATGGCTGCGA GCCCTGCGGG
1081 AACGACACCT TCAACCGAGA GCCAGCCATT GTCAGGTTCT TCTCCCGGTT CACAGAGGTC
1141 AGGGAGTTTG CCATTGTTCC CCTGCATGCG GCCCCGGGGG ACGCAGTAGC CGAGATCGAC
1201 GCTCTCTATG ACGTCTACCT GGATGTCCAA GAGAAATGGG GCTTGAGGA CGTCATGTTG
1261 ATGGGCGACT TCAATGCGGG CTGCAGCTAT GTGAGACCTT CCCAGTGGTC ATCCATCCGC
1321 CTGTGGACAA GCCCCACCTT CCAGTGGCTG ATCCCCGACA GCGCTGACAC CACAGCTACA
1381 CCCACGCACT GTGCCTATGA CAGGATCGTG GTTGCAGGGA TGCTGCTCCG AGGGGCCGTT
1441 GTTCCCGACT CGGCTCTTCC CTTTAACTTC CAGGCTGCCT ATGGCCTGAG TGACCAACTG
1501 GCCCAAGCCA TCAGTGACCA CTATCCAGTG GAGGTGATGC TGAAGGGGGG CGGACCCAAA
1561 AAGAAGCGCA AGGTTTGA
```

//

Fig. 17(B)



LOCUS FDDNASE105 1587 BP SS-DNA SYN 29-AUG-2000
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -
FEATURES Location/Qualifiers
frag 10..1587
/note="1 to 1578 of FdDNase105correct"
frag join(10..>729,<790..1587)
/note="1 to 1578 of PAS105.dna [Split]"
frag 730..789
/note="1 to 60 of 101/105linker"
frag join(730..>744,<745..>768,<769..>789)
/note="1 to 80 of 102linker [Split]"
BASE COUNT 354 A 477 C 445 G 311 T 0 OTHER
ORIGIN -
1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCTT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTCG
541 TGGAACTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCTT ACAGTCCTCA
601 GGA CTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTGTG ACAA AACTCA CACATGTCCA CCGTGTCCAG CACCAGAGGG CGGGCTGAAG
781 ATCGCAGCCT TCAACATCCA GACATTTGGG GAGACCAAGA TGTCCAATGC CACCCCTCGTC
841 AGCTACATTG TGCAGATCCT GAGCCGCTAC GACATCGCCC TGGTCCAGGA GGTCAGAGAC
901 AGCCACCTGA CTGCCGTGGG GAAGCTGCTG GACAACCTCA ATCAGGACGC ACCAGACACC
961 TATCACTACG TGGTCAGTGA GCCACTGGGA CGGAACAGCT ATAAGGAGCG CTACCTGTTC
1021 GTGTACAGGC CTGACCAGGT GTCTGCGGTG GACAGCTACT ACTACGATGA TGGCTGCGAG
1081 CCCTGCGGGA ACGACACCTT CAACCGAGAG CCAGCCATTG TCAGGTTCTT CTCCCGGTTT
1141 ACAGAGGTCA GGGAGTTTGC CATTGTTCCC CTGCATGCGG CCCC GG GGA CGCAGTAGCC
1201 GAGATCGACG CTCTCTATGA CGTCTACCTG GATGTCCAAG AGAAATGGGG CTGGGAGGAC
1261 GTCATGTTGA TGGGCGACTT CAATGCGGGC TGCAGCTATG TGAGACCTC CCAGTGGTCA
1321 TCCATCCGCC TGTGGACAAG CCCCACCTT CAGTGGCTGA TCCCCGACAG CGCTGACACC
1381 ACAGCTACAC CCACGCACTG TGCCTATGAC AGGATCGTGG TTGCAGGGAT GCTGCTCCGA
1441 GGGGCCGTTG TTCCCGACTC GGCTCTTCCC TTTAACTTCC AGGCTGCCTA TGGCCTGAGT
1501 GACCAACTGG CCAAGCCAT CAGTGACCAC TATCCAGTGG AGGTGATGCT GAAGGGGGGC
1561 GGACCCAAAA AGAAGCGCAA GGTTTGA

//

Fig. 17(C)

54
GTC CAC
V H

Fig. 17(D)
(Sheet 1 of 3)

		603				612				621				630				639				648	
CTC	TAC	TCC	CTC	AGC	AGC	GTG	GTG	ACC	GTG	CCC	TCC	AGC	AGC	TTG	GGC	ACC	CAG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
L	Y	S	L	S	S	V	V	T	V	P	S	S	S	L	G	T	Q						
		657				666				675				684				693				702	
ACC	TAC	ATC	TGC	AAC	GTG	AAT	CAC	AAG	CCC	AGC	AAC	ACC	AAG	GTG	GAC	AAG	AAA						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
T	Y	I	C	N	V	N	H	K	P	S	N	T	K	V	D	K	K						
		711				720				729				738				747				756	
GTT	GAG	CCC	AAA	TCT	TGT	GAC	AAA	ACT	CAC	ACA	TGC	CCA	CCG	TGC	CCA	GCA	CCT						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
V	E	P	K	S	C	D	K	T	H	T	C	P	P	C	P	A	P						
		765				774				783				792				801				810	
GAA	GGC	GGG	CTG	AAG	ATC	GCA	GCC	TTC	AAC	ATC	CAG	ACA	TTT	GGG	GAG	ACC	AAG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
E	G	G	L	K	I	A	A	F	N	I	Q	T	F	G	E	T	K						
		819				828				837				846				855				864	
ATG	TCC	AAT	GCC	ACC	CTC	GTC	AGC	TAC	ATT	GTG	CAG	ATC	CTG	AGC	CGC	TAC	GAC						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
M	S	N	A	T	L	V	S	Y	I	V	Q	I	L	S	R	Y	D						
		873				882				891				900				909				918	
ATC	GCC	CTG	GTC	CAG	GAG	GTC	AGA	GAC	AGC	CAC	CTG	ACT	GCC	GTG	GGG	AAG	CTG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
I	A	L	V	Q	E	V	R	D	S	H	L	T	A	V	G	K	L						
		927				936				945				954				963				972	
CTG	GAC	AAC	CTC	AAT	CAG	GAC	GCA	CCA	GAC	ACC	TAT	CAC	TAC	GTG	GTC	AGT	GAG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
L	D	N	L	N	Q	D	A	P	D	T	Y	H	Y	V	V	S	E						
		981				990				999				1008				1017				1026	
CCA	CTG	GGA	CGG	AAC	AGC	TAT	AAG	GAG	CGC	TAC	CTG	TTG	GTG	TAC	AGG	CCT	GAC						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
P	L	G	R	N	S	Y	K	E	R	Y	L	F	V	Y	R	P	D						
		1035				1044				1053				1062				1071				1080	
CAG	GTG	TCT	GCG	GTG	GAC	AGC	TAC	TAC	TAC	GAT	GAT	GGC	TGC	GAG	CCC	TGC	GGG						
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---						
Q	V	S	A	V	D	S	Y	Y	Y	D	D	G	C	E	P	C	G						

Fig. 17(D)
(Sheet 2 of 3)



```

GCC GAG ATC GAC GCT CTC TAT GAC GTC TAC CTG GAT GTC CAA GAG AAA TGG GGC
---
A E I D A L Y D V Y L D V Q E K W G

      1251      1260      1269      1278      1287      1296
TTG GAG GAC GTC ATG TTG ATG GGC GAC TTC AAT GCG GGC TGC AGC TAT GTG AGA
---
L E D V M L M G D F N A G C S Y V R

      1305      1314      1323      1332      1341      1350
CCC TCC CAG TGG TCA TCC ATC CGC CTG TGG ACA AGC CCC ACC TTC CAG TGG CTG
---
P S Q W S S I R L W T S P T F Q W L

      1359      1368      1377      1386      1395      1404
ATC CCC GAC AGC GCT GAC ACC ACA GCT ACA CCC ACG CAC TGT GCC TAT GAC AGG
---
I P D S A D T T A T P T H C A Y D R

      1413      1422      1431      1440      1449      1458
ATC GTG GTT GCA GGG ATG CTG CTC CGA GGG GCC GTT GTT CCC GAC TCG GCT CTT
---
I V V A G M L L R G A V V P D S A L

      1467      1476      1485      1494      1503      1512
CCC TTT AAC TTC CAG GCT GCC TAT GGC CTG AGT GAC CAA CTG GCC CAA GCC ATC
---
P F N F Q A A Y G L S D Q L A Q A I

      1521      1530      1539      1548      1557      1566
AGT GAC CAC TAT CCA GTG GAG GTG ATG CTG AAG GGG GGC GGA CCC AAA AAG AAG
---
S D H Y P V E V M L K G G G P K K K

      1575
CGC AAG GTT TGA 3'
---
R K V *
```

Fig. 17(D)
(Sheet 3 of 3)

pAS106

LOCUS PAS106.DNA 1596 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS (pAS106)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 355 a 475 c 452 g 314 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG **TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGGAGCGGC**
781 **GGG**CTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCACTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTCTG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCAGAGAG CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAAGTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGGGGGGCG **GACCCAAAAA GAAGCGCAAG GTTTGA**

//

→ NLS

Fig. 18(A)

25 AUG 2000

LOCUS FDDNASE106 1596 BP SS-DNA SYN

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES

frag Location/Qualifiers
join(1..>720,<799..1596)
/note="1 to 1596 of PAS106.dna [Split]"

frag
721..798
/note="1 to 78 of 102/106linker"

BASE COUNT 355 A 474 C 452 G 315 T 0 OTHER

ORIGIN -

```

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTG GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAACCT ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGGAGCGGC
781 GGGCTGAAGA TCGCAGCCTT CAACATCCAG ACATTTGGGG AGACCAAGAT GTCCAATGCC
841 ACCCTCGTCA GCTACATTGT GCAGATCCTG AGCCGCTACG ACATCGCCCT GGTCCAGGAG
901 GTCAGAGACA GCCACCTGAC TGCCGTGGGG AAGCTGCTGG ACAACCTCAA TCAGGACGCA
961 CCAGACACCT ATCACTACGT GGTCAGTGAG CCACTGGGAC GGAACAGCTA TAAGGAGCGC
1021 TACCTGTTTG TGTACAGGCC TGACCAGGTG TCTGCGGTGG ACAGCTACTA CTACGATGAT
1081 GGCTGCGAGC CCTGCGGGAA CGACACCTTC AACCGAGAGC CAGCCATTGT CAGGTTCTTC
1141 TCCCGGTTCA CAGAGGTCAG GGAGTTTGCC ATTGTTCCCC TGCATGCGGC CCCGGGGGAC
1201 GCAGTAGCCG AGATCGACGC TCTCTATGAC GTCTACCTGG ATGTCCAAGA GAAATGGGGC
1261 TTGGAGGACG TCATGTTGAT GGGCGACTTC AATGCGGGCT GCAGCTATGT GAGACCCTCC
1321 CAGTGGTCAT CCATCCGCCT GTGGACAAGC CCCACCTTCC AGTGGCTGAT CCCCACAGC
1381 GCTGACACCA CAGCTACACC CACGCACTGT GCCTATGACA GGATCGTGGT TGCAGGGATG
1441 CTGCTCCGAG GGGCCGTTGT TCCCGACTCG GCTCTTCCCT TTAAGTTCCA GGCTGCCTAT
1501 GGCCTGAGTG ACCAACTGGC CCAAGCCATC AGTGACCACT ATCCAGTGGA GGTGATGCTG
1561 AAGGGGGGCG GACCCAAAAA GAAGCGCAAG GTTTGA

```

//

Fig. 18(B)

LOCUS FDDNASE106 1605 BP SS-DNA SYN 29-AUG-2000
 DEFINITION -
 ACCESSION -
 KEYWORDS -
 SOURCE -

FEATURES Location/Qualifiers
 frag 10..1605
 /note="1 to 1596 of FdDNase106correct"
 frag join(10..>729,<808..1605)
 /note="1 to 1596 of PAS106.dna [Split]"
 frag 730..807
 /note="1 to 78 of 102/106linker"

BASE COUNT 356 A 480 C 454 G 315 T 0 OTHER
 ORIGIN -

1 GCGGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
 61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
 121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
 181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
 241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
 301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
 361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCCTCA
 421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
 481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
 541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCTCTCA
 601 GGA CTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
 661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
 721 AAATCTTGTG ACAA AACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
 781 GGGAGCGGCG GGCTGAAGAT CGCAGCCTTC AACATCCAGA CATTGGGGA GACCAAGATG
 841 TCCAATGCCA CCCTCGTCAG CTACATTGTG CAGATCCTGA GCCGCTACGA CATCGCCCTG
 901 GTCCAGGAGG TCAGAGACAG CCACCTGACT GCCGTGGGGA AGCTGCTGGA CAACCTCAAT
 961 CAGGACGCAC CAGACACCTA TCACTACGTG GTCAGTGAGC CACTGGGACG GAACAGCTAT
 1021 AAGGAGCGCT ACCTGTTCGT GTACAGGCCT GACCAGGTGT CTGCGGTGGA CAGCTACTAC
 1081 TACGATGATG GCTGCGAGCC CTGCGGGAAC GACACCTTCA ACCGAGAGCC AGCCATTGTC
 1141 AGGTTCTTCT CCCGTTTAC AGAGGTGAGG GAGTTTGCCA TTGTTCCCTT GCATGCGGCC
 1201 CCGGGGGACG CAGTAGCCGA GATCGACGCT CTCTATGACG TCTACCTGGA TGTCCAAGAG
 1261 AAATGGGGCT TGGAGGACGT CATGTTGATG GGCGACTTCA ATGCGGGCTG CAGCTATGTG
 1321 AGACCTTCCC AGTGGTCATC CATCCGCCTG TGGACAAGCC CCACCTTCCA GTGGCTGATC
 1381 CCCGACAGCG CTGACACCAC AGCTACACCC ACGCACTGTG CCTATGACAG GATCGTGGTT
 1441 GCAGGGATGC TGCTCCGAGG GGCCGTTGTT CCCGACTCGG CTCTTCCCTT TAACTTCCAG
 1501 GCTGCCTATG GCCTGAGTGA CCAACTGGCC CAAGCCATCA GTGACCACTA TCCAGTGGAG
 1561 GTGATGCTGA AGGGGGGCGG ACCCAAAAAG AAGCGCAAGG TTTGA

//

Fig. 18(C)

		9			18			27			36						45				54
ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H				
		63			72			81			90			99			108				
TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S				
		117			126			135			144			153			162				
GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E				
		171			180			189			198			207			216				
TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P				
		225			234			243			252			261			270				
GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T				
		279			288			297			306			315			324				
AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E				
		333			342			351			360			369			378				
GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y				
		387			396			405			414			423			432				
TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S				
		441			450			459			468			477			486				
GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L				
		495			504			513			522			531			540				
GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA				
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---				
G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S				

Fig. 18(D)

(Sheet 1 of 3)

GCC	CCG	GGG	GAC	GCA	GTA	GCC	GAG	ATC	GAC	GCT	CTC	TAT	GAC	GTC	TAC	CTG	GAT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
A	P	G	D	A	V	A	E	I	D	A	L	Y	D	V	Y	L	D
		1251			1260			1269			1278			1287			1296
GTC	CAA	GAG	AAA	TGG	GGC	TTG	GAG	GAC	GTC	ATG	TTG	ATG	GGC	GAC	TTC	AAT	GCG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	Q	E	K	W	G	L	E	D	V	M	L	M	G	D	F	N	A
		1305			1314			1323			1332			1341			1350
GGC	TGC	AGC	TAT	GTG	AGA	CCC	TCC	CAG	TGG	TCA	TCC	ATC	CGC	CTG	TGG	ACA	AGC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	C	S	Y	V	R	P	S	Q	W	S	S	I	R	L	W	T	S
		1359			1368			1377			1386			1395			1404
CCC	ACC	TTC	CAG	TGG	CTG	ATC	CCC	GAC	AGC	GCT	GAC	ACC	ACA	GCT	ACA	CCC	ACG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
P	T	F	Q	W	L	I	P	D	S	A	D	T	T	A	T	P	T
		1413			1422			1431			1440			1449			1458
CAC	TGT	GCC	TAT	GAC	AGG	ATC	GTG	GTT	GCA	GGG	ATG	CTG	CTC	CGA	GGG	GCC	GTT
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
H	C	A	Y	D	R	I	V	V	A	G	M	L	L	R	G	A	V
		1467			1476			1485			1494			1503			1512
GTT	CCC	GAC	TCG	GCT	CTT	CCC	TTT	AAC	TTC	CAG	GCT	GCC	TAT	GGC	CTG	AGT	GAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
V	P	D	S	A	L	P	F	N	F	Q	A	A	Y	G	L	S	D
		1521			1530			1539			1548			1557			1566
CAA	CTG	GCC	CAA	GCC	ATC	AGT	GAC	CAC	TAT	CCA	GTG	GAG	GTG	ATG	CTG	AAG	GGG
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
Q	L	A	Q	A	I	S	D	H	Y	P	V	E	V	M	L	K	G
		1575			1584			1593									
GGC	GGA	CCC	AAA	AAG	AAG	CGC	AAG	GTT	TGA	3'							
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
G	G	P	K	K	K	R	K	V	*								

Fig. 18(D)

(Sheet 3 of 3)



pAS107


LOCUS PAS107.DNA 1590 bp mRNA PRI 06-MAR-1995
DEFINITION Humanised HMFG1 Fab'2 fused to human DNase I with SV40
NLS (pAS107)
ACCESSION
NID
KEYWORDS DNase I.
SOURCE DNase I sequence is from assembled oligos (thus modified c/f
MHDNASE1.dna)
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS Shak, S., Capon, D.J., Hellmiss, R., Marsters, S.A. and Baker, C.L.
TITLE Recombinant human DNase I reduces the viscosity of cystic
fibrosis
sputum
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (23), 9188-9192 (1990)
MEDLINE 91067672
BASE COUNT 354 a 474 c 448 g 314 t
ORIGIN

1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
121 TGCAAGGCTT CTGGCTACAC CTTCAAGTGG TACTGGATAG AGTGGGTGCG CCAGGCTCCA
181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATACAAT
241 GAGAAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
361 TTTGCCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
421 AAGGGCCCAT CGGTCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAAGTCA
541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
661 AACGTGAATC ACAAGCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
721 GACAAAATC ACACATGCTG TGTGGAGTGC CCACCGTGCC CAGCACCTGA AGGCGGGCTG
781 AAGATCGCAG CTTTCAACAT CCAGACATT GGGGAGACCA AGATGTCCAA TGCCACCCTC
841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
901 GACAGCCACC TGAAGTCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTGAGGTT CTTCTCCCGG
1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCGGGG GGACGCAGTA
1201 GCCGAGATCG ACGTCTCTTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGCG TGATCCCCGA CAGCGCTGAC
1381 ACCACAGTA CACCCACGCA CTGTGCCAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA

//

└─→ NLS

Fig. 19(A)



```

LOCUS      FDDNASE107      1590 BP SS-DNA      SYN      25-AUG-2000
DEFINITION -
ACCESSION  -
KEYWORDS   -
SOURCE     -
FEATURES   Location/Qualifiers
            frag      join(1..>720,<793..1590)
                        /note="1 to 1590 of PAS107.dna [Split]"
            frag      721..792
                        /note="1 to 72 of 103/107linker"
            frag      join(721..>771,<772..792)
                        /note="1 to 78 of 102linker [Split]"
BASE COUNT      354 A      473 C      448 G      315 T      0 OTHER
ORIGIN      -
            1 ATGGGATGGA GCTGTATCAT CCTCTTCTTG GTAGCAACAG CTACAGGTGT CCACTCCCAG
              61 GTGCAGCTGG TGCAGTCTGG GGCAGAGGTG AAAAAGCCTG GGGCCTCAGT GAAGGTGTCC
            121 TGCAAGGCTT CTGGCTACAC CTTCAGTGCC TACTGGATAG AGTGGGTGCG CCAGGCTCCA
            181 GGAAAGGGCC TCGAGTGGGT CGGAGAGATT TTACCTGGAA GTAATAATTC TAGATAACAAT
            241 GAGAAGTTCA AGGGCCGAGT GACAGTCACT AGAGACACAT CCACAAACAC AGCCTACATG
            301 GAGCTCAGCA GCCTGAGGTC TGAGGACACA GCCGTCTATT ACTGTGCAAG ATCCTACGAC
            361 TTTGCTGGT TTGCTTACTG GGGCCAAGGG ACTCTGGTCA CAGTCTCCTC AGCCTCCACC
            421 AAGGGCCCAT CGGTCCTTCCC CCTGGCACCC TCCTCCAAGA GCACCTCTGG GGGCACAGCG
            481 GCCCTGGGCT GCCTGGTCAA GGACTACTTC CCCGAACCGG TGACGGTGTC GTGGAATCA
            541 GGCGCCCTGA CCAGCGGCGT GCACACCTTC CCGGCTGTCC TACAGTCCTC AGGACTCTAC
            601 TCCCTCAGCA GCGTGGTGAC CGTGCCCTCC AGCAGCTTGG GCACCCAGAC CTACATCTGC
            661 AACGTGAATC ACAAGCCCAG CAACACCAAG GTGGACAAGA AAGTTGAGCC CAAATCTTGT
            721 GACAAAATC ACACATGCTG TGTCGAGTGT CCACCGTGTC CAGCACCAGA GGGCGGGCTG
            781 AAGATCGCAG CCTTCAACAT CCAGACATTT GGGGAGACCA AGATGTCCAA TGCCACCCTC
            841 GTCAGCTACA TTGTGCAGAT CCTGAGCCGC TACGACATCG CCCTGGTCCA GGAGGTCAGA
            901 GACAGCCACC TGA CTGCCGT GGGGAAGCTG CTGGACAACC TCAATCAGGA CGCACCAGAC
            961 ACCTATCACT ACGTGGTCAG TGAGCCACTG GGACGGAACA GCTATAAGGA GCGCTACCTG
           1021 TTCGTGTACA GGCCTGACCA GGTGTCTGCG GTGGACAGCT ACTACTACGA TGATGGCTGC
           1081 GAGCCCTGCG GGAACGACAC CTTCAACCGA GAGCCAGCCA TTGTCAGGTT CTTCTCCCGG
           1141 TTCACAGAGG TCAGGGAGTT TGCCATTGTT CCCCTGCATG CGGCCCCGGG GGACGCAGTA
           1201 GCCGAGATCG ACGCTCTCTA TGACGTCTAC CTGGATGTCC AAGAGAAATG GGGCTTGGAG
           1261 GACGTCATGT TGATGGGCGA CTTCAATGCG GGCTGCAGCT ATGTGAGACC CTCCCAGTGG
           1321 TCATCCATCC GCCTGTGGAC AAGCCCCACC TTCCAGTGGC TGATCCCCGA CAGCGCTGAC
           1381 ACCACAGCTA CACCCACGCA CTGTGCCTAT GACAGGATCG TGGTTGCAGG GATGCTGCTC
           1441 CGAGGGGCGG TTGTTCCCGA CTCGGCTCTT CCCTTTAACT TCCAGGCTGC CTATGGCCTG
           1501 AGTGACCAAC TGGCCCAAGC CATCAGTGAC CACTATCCAG TGGAGGTGAT GCTGAAGGGG
           1561 GGCGGACCCA AAAAGAAGCG CAAGGTTTGA
  
```

//

Fig. 19(B)



LOCUS FDDNASE107 1599 BP SS-DNA SYN 29-AUG-2000
DEFINITION -
ACCESSION -
KEYWORDS -
SOURCE -
FEATURES Location/Qualifiers
frag 10..1599
/note="1 to 1590 of FdDNase107correct"
frag join(10..>729,<802..1599)
/note="1 to 1590 of PAS107.dna [Split]"
frag 730..801
/note="1 to 72 of 103/107linker"
frag join(730..>780,<781..801)
/note="1 to 78 of 102linker [Split]"
BASE COUNT 355 A 479 C 450 G 315 T 0 OTHER
ORIGIN -
1 GCCGCCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG TAGCAACAGC TACAGGTGTC
61 CACTCCCAGG TGCAGCTGGT GCAGTCTGGG GCAGAGGTGA AAAAGCCTGG GGCCTCAGTG
121 AAGGTGTCCT GCAAGGCTTC TGGCTACACC TTCAGTGCCT ACTGGATAGA GTGGGTGCGC
181 CAGGCTCCAG GAAAGGGCCT CGAGTGGGTC GGAGAGATTT TACCTGGAAG TAATAATTCT
241 AGATACAATG AGAAGTTCAA GGGCCGAGTG ACAGTCACTA GAGACACATC CACAAACACA
301 GCCTACATGG AGCTCAGCAG CCTGAGGTCT GAGGACACAG CCGTCTATTA CTGTGCAAGA
361 TCCTACGACT TTGCCTGGTT TGCTTACTGG GGCCAAGGGA CTCTGGTCAC AGTCTCTCA
421 GCCTCCACCA AGGGCCCATC GGTCTTCCCC CTGGCACCCCT CCTCCAAGAG CACCTCTGGG
481 GGCACAGCGG CCCTGGGCTG CCTGGTCAAG GACTACTTCC CCGAACCGGT GACGGTGTGCG
541 TGGAACCTCAG GCGCCCTGAC CAGCGGCGTG CACACCTTCC CGGCTGTCCT ACAGTCTCTCA
601 GGA CTCTACT CCCTCAGCAG CGTGGTGACC GTGCCCTCCA GCAGCTTGGG CACCCAGACC
661 TACATCTGCA ACGTGAATCA CAAGCCCAGC AACACCAAGG TGGACAAGAA AGTTGAGCCC
721 AAATCTTG TG ACAA AACTCA CACATGCTGT GTCGAGTGTC CACCGTGTCC AGCACCAGAG
781 GCGGGGCTGA AGATCGCAGC CTTCAACATC CAGACATTG GGGAGACCAA GATGTCCAAT
841 GCCACCCTCG TCAGCTACAT TGTGCAGATC CTGAGCCGCT ACGACATCGC CCTGGTCCAG
901 GAGGTCAGAG ACAGCCACCT GACTGCCGTG GGGAAAGCTGC TGGACAACCT CAATCAGGAC
961 GCACCAGACA CCTATCACTA CGTGGTCAAGT GAGCCACTGG GACGGAACAG CTATAAGGAG
1021 CGCTACCTGT TCGTGTACAG GCCTGACCAG GTGTCTGCGG TGGACAGCTA CTACTACGAT
1081 GATGGCTGCG AGCCCTGCGG GAACGACACC TTCAACCGAG AGCCAGCCAT TGTCAGGTTT
1141 TTCTCCCGGT TCACAGAGGT CAGGGAGTTT GCCATTGTTC CCCTGCATGC GGCCCCGGGG
1201 GACGCAGTAG CCGAGATCGA CGCTCTCTAT GACGTCTACC TGGATGTCCA AGAGAAATGG
1261 GGCTTGAGG ACGTCATGTT GATGGGCGAC TTCAATGCGG GCTGCAGCTA TGTGAGACCC
1321 TCCCAGTGGT CATCCATCCG CCTGTGGACA AGCCCCACCT TCCAGTGGCT GATCCCCGAC
1381 AGCGCTGACA CCACAGCTAC ACCACGCAC TGTGCCTATG ACAGGATCGT GGTGTCAGGG
1441 ATGCTGCTCC GAGGGGCCGT TGTTCCTGAC TCGGCTCTTC CCTTTAACTT CCAGGCTGCC
1501 TATGGCCTGA GTGACCAACT GGCCCCAAGCC ATCAGTGACC ACTATCCAGT GGAGGTGATG
1561 CTGAAGGGGG GCGGACCCAA AAAGAAGCGC AAGGTTTGA

//

Fig. 19(C)

5'	ATG	GGA	TGG	AGC	TGT	ATC	ATC	CTC	TTC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	GTC	CAC
	M	G	W	S	C	I	I	L	F	L	V	A	T	A	T	G	V	H
	TCC	CAG	GTG	CAG	CTG	GTG	CAG	TCT	GGG	GCA	GAG	GTG	AAA	AAG	CCT	GGG	GCC	TCA
	S	Q	V	Q	L	V	Q	S	G	A	E	V	K	K	P	G	A	S
	GTG	AAG	GTG	TCC	TGC	AAG	GCT	TCT	GGC	TAC	ACC	TTC	AGT	GCC	TAC	TGG	ATA	GAG
	V	K	V	S	C	K	A	S	G	Y	T	F	S	A	Y	W	I	E
	TGG	GTG	CGC	CAG	GCT	CCA	GGA	AAG	GGC	CTC	GAG	TGG	GTC	GGA	GAG	ATT	TTA	CCT
	W	V	R	Q	A	P	G	K	G	L	E	W	V	G	E	I	L	P
	GGA	AGT	AAT	AAT	TCT	AGA	TAC	AAT	GAG	AAG	TTC	AAG	GGC	CGA	GTG	ACA	GTC	ACT
	G	S	N	N	S	R	Y	N	E	K	F	K	G	R	V	T	V	T
	AGA	GAC	ACA	TCC	ACA	AAC	ACA	GCC	TAC	ATG	GAG	CTC	AGC	AGC	CTG	AGG	TCT	GAG
	R	D	T	S	T	N	T	A	Y	M	E	L	S	S	L	R	S	E
	GAC	ACA	GCC	GTC	TAT	TAC	TGT	GCA	AGA	TCC	TAC	GAC	TTT	GCC	TGG	TTT	GCT	TAC
	D	T	A	V	Y	Y	C	A	R	S	Y	D	F	A	W	F	A	Y
	TGG	GGC	CAA	GGG	ACT	CTG	GTC	ACA	GTC	TCC	TCA	GCC	TCC	ACC	AAG	GGC	CCA	TCG
	W	G	Q	G	T	L	V	T	V	S	S	A	S	T	K	G	P	S
	GTC	TTC	CCC	CTG	GCA	CCC	TCC	TCC	AAG	AGC	ACC	TCT	GGG	GGC	ACA	GCG	GCC	CTG
	V	F	P	L	A	P	S	S	K	S	T	S	G	G	T	A	A	L
	GGC	TGC	CTG	GTC	AAG	GAC	TAC	TTC	CCC	GAA	CCG	GTG	ACG	GTG	TCG	TGG	AAC	TCA
	G	C	L	V	K	D	Y	F	P	E	P	V	T	V	S	W	N	S
	GGC	GCC	CTG	ACC	AGC	GGC	GTG	CAC	ACC	TTC	CCG	GCT	GTC	CTA	CAG	TCC	TCA	GGA
	G	A	L	T	S	G	V	H	T	F	P	A	V	L	Q	S	S	G

Fig. 19(D)
(Sheet 1 of 3)

603	612	621	630	639	648
CTC TAC TCC CTC AGC AGC GTG GTG ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG					
L Y S L S S V V T V P S S S L G T Q					
657	666	675	684	693	702
ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AAA					
T Y I C N V N H K P S N T K V D K K					
711	720	729	738	747	756
GTT GAG CCC AAA TCT TGT GAC AAA ACT CAC ACA TGC TGT GTG GAG TGC CCA CCG					
V E P K S C D K T H T C C V E C P P					
765	774	783	792	801	810
TGC CCA GCA CCT GAA GGC GGG CTG AAG ATC GCA GCC TTC AAC ATC CAG ACA TTT					
C P A P E G G L K I A A F N I Q T F					
819	828	837	846	855	864
GGG GAG ACC AAG ATG TCC AAT GCC ACC CTC GTC AGC TAC ATT GTG CAG ATC CTG					
G E T K M S N A T L V S Y I V Q I L					
873	882	891	900	909	918
AGC CGC TAC GAC ATC GCC CTG GTC CAG GAG GTC AGA GAC AGC CAC CTG ACT GCC					
S R Y D I A L V Q E V R D S H L T A					
927	936	945	954	963	972
GTG GGG AAG CTG CTG GAC AAC CTC AAT CAG GAC GCA CCA GAC ACC TAT CAC TAC					
V G K L L D N L N Q D A P D T Y H Y					
981	990	999	1008	1017	1026
GTG GTC AGT GAG CCA CTG GGA CGG AAC AGC TAT AAG GAG CGC TAC CTG TTC GTG					
V V S E P L G R N S Y K E R Y L F V					
1035	1044	1053	1062	1071	1080
TAC AGG CCT GAC CAG GTG TCT GCG GTG GAC AGC TAC TAC TAC GAT GAT GGC TGC					
Y R P D Q V S A V D S Y Y Y D D G C					
1089	1098	1107	1116	1125	1134
GAG CCC TGC GGG AAC GAC ACC TTC AAC CGA GAG CCA GCC ATT GTC AGG TTC TTC					
E P C G N D T F N R E P A I V R F F					
1143	1152	1161	1170	1179	1188
TCC CGG TTC ACA GAG GTC AGG GAG TTT GCC ATT GTT CCC CTG CAT GCG GCC CCG					
S R F T E V R E F A I V P L H A A P					
1197	1206	1215	1224	1233	1242

Fig. 19(D)
(Sheet 2 of 3)

Fig. 19(D)
(Sheet 3 of 3)

Mammalian expression of humanised HMFG1-D Nase constructs

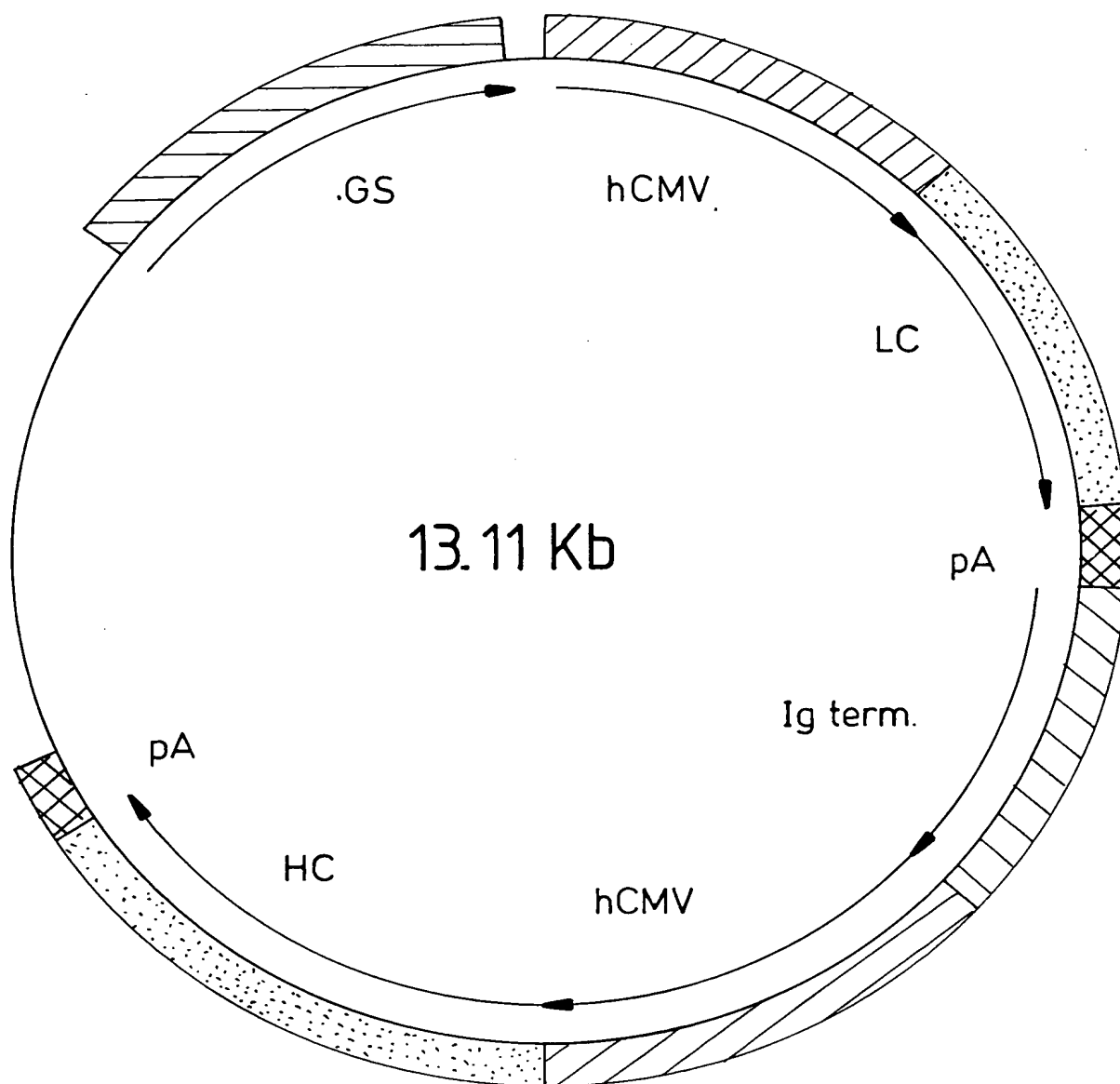
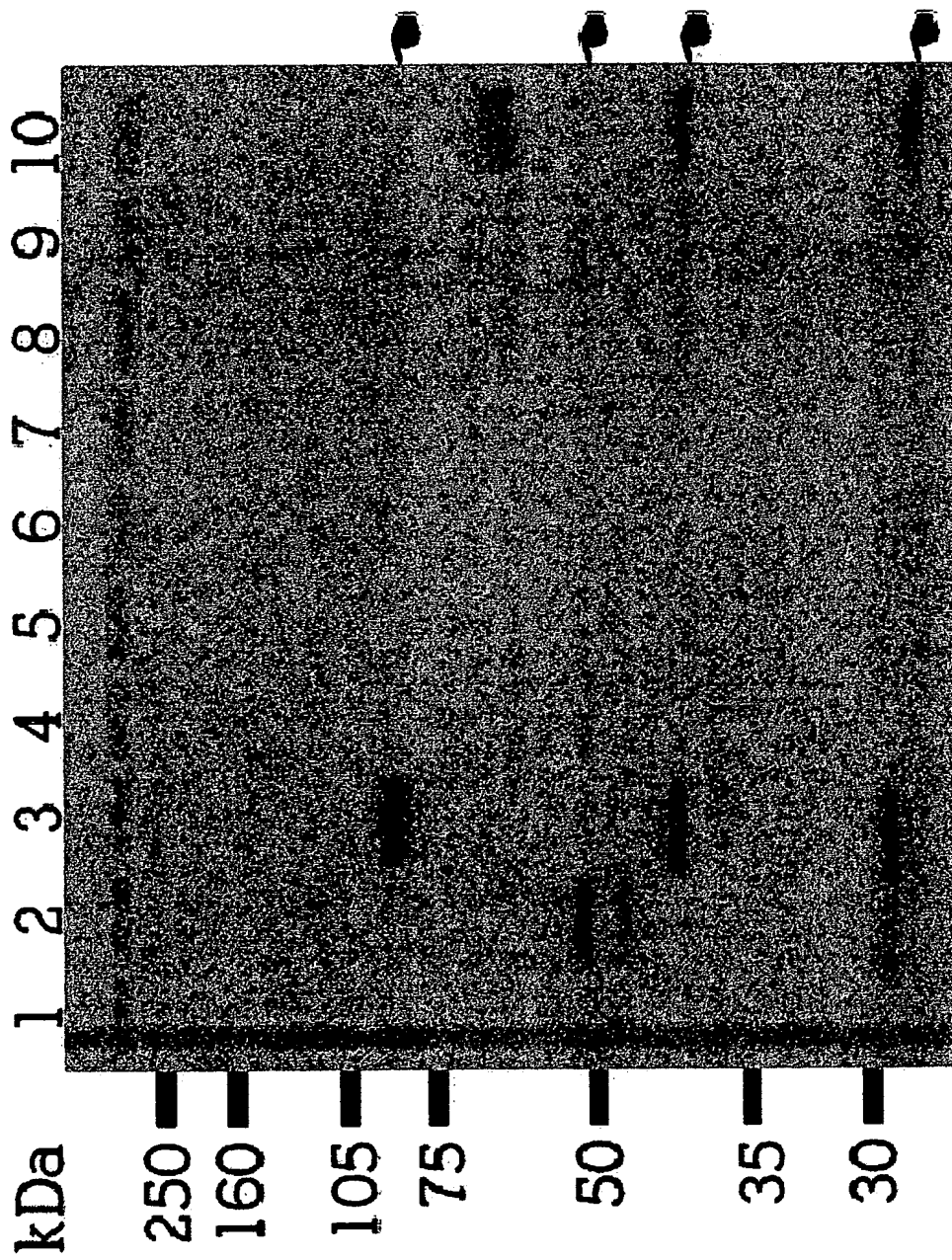


Fig. 20

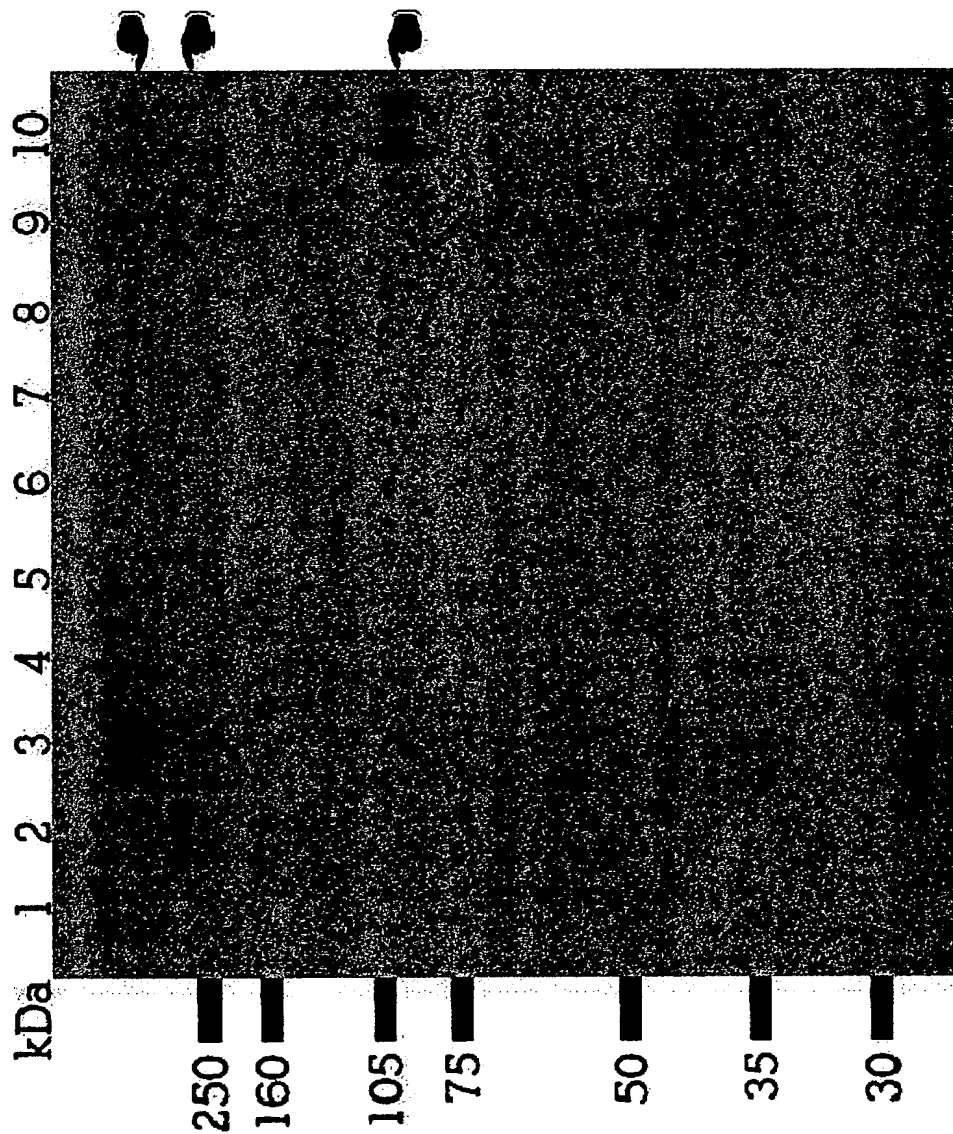
Immuno-precipitation of metabolically labelled transient transfectants



8% SDS-PAGE reducing gel

Fig. 21(A)

Immuno-precipitation of metabolically labelled transient transfectants

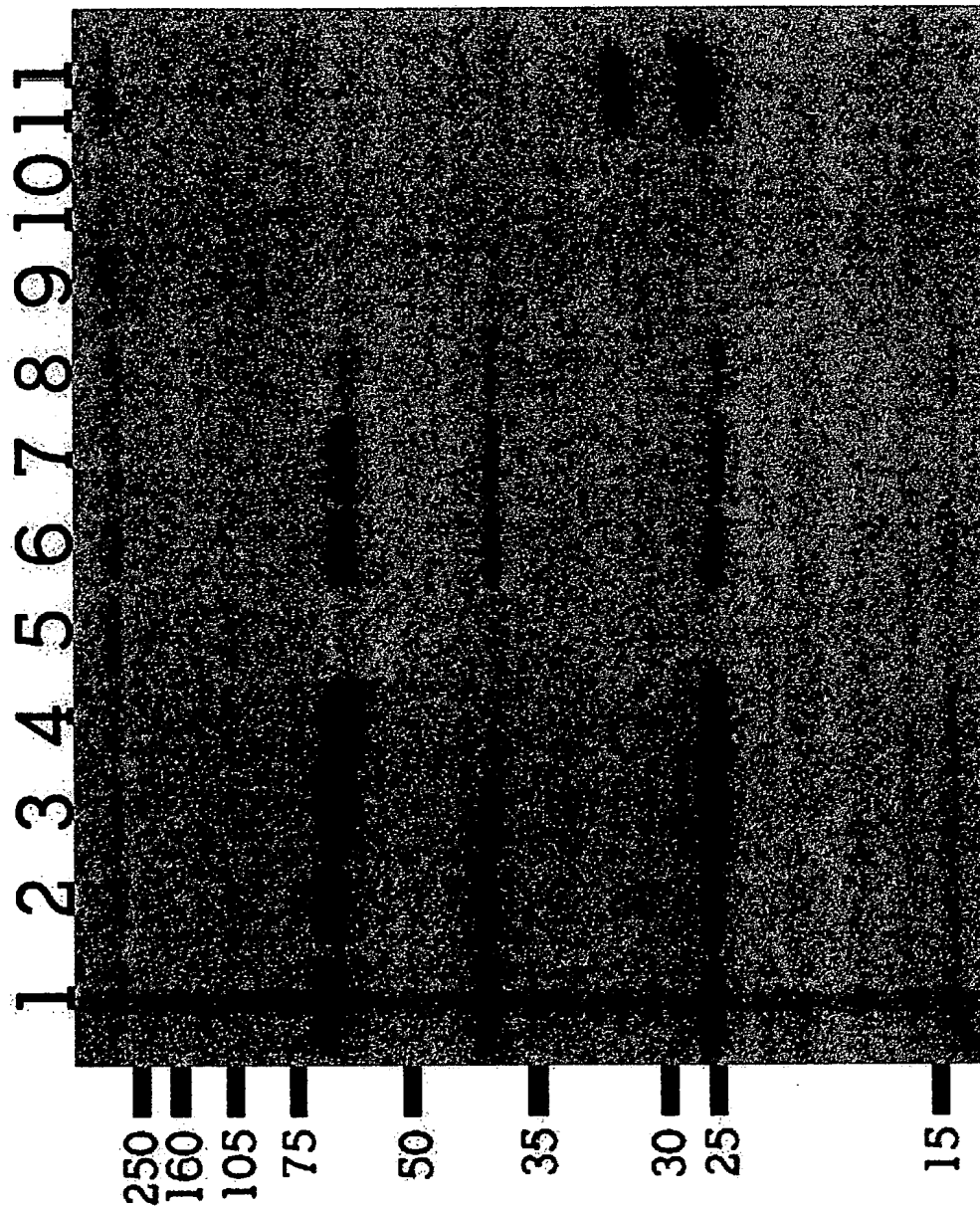


8% SDS-PAGE non-reducing gel

Fig. 21(B)

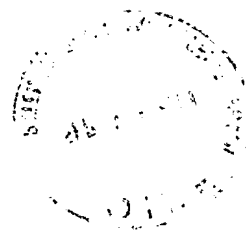


Immuno-precipitation of metabolically labelled transient transfectants



10% SDS-PAGE reducing gel

Fig. 21(C)



Immuno-precipitation of metabolically labelled transient transfectants

1 2 3 4 5 6 7 8 9 10 11

kDa

250

160

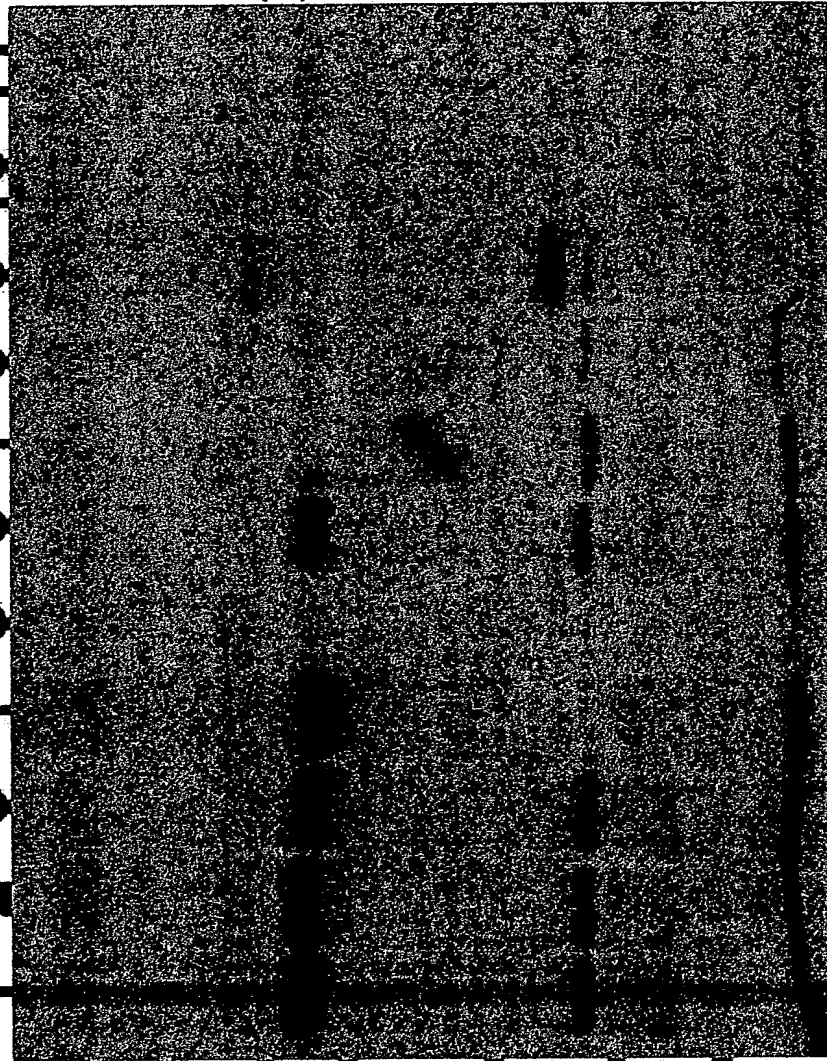
105

75

50

35

30



8% SDS-PAGE non-reducing gel

Fig. 21(D)



Fig. 22

**PDTRP binding assay standard curve
(5' development)**

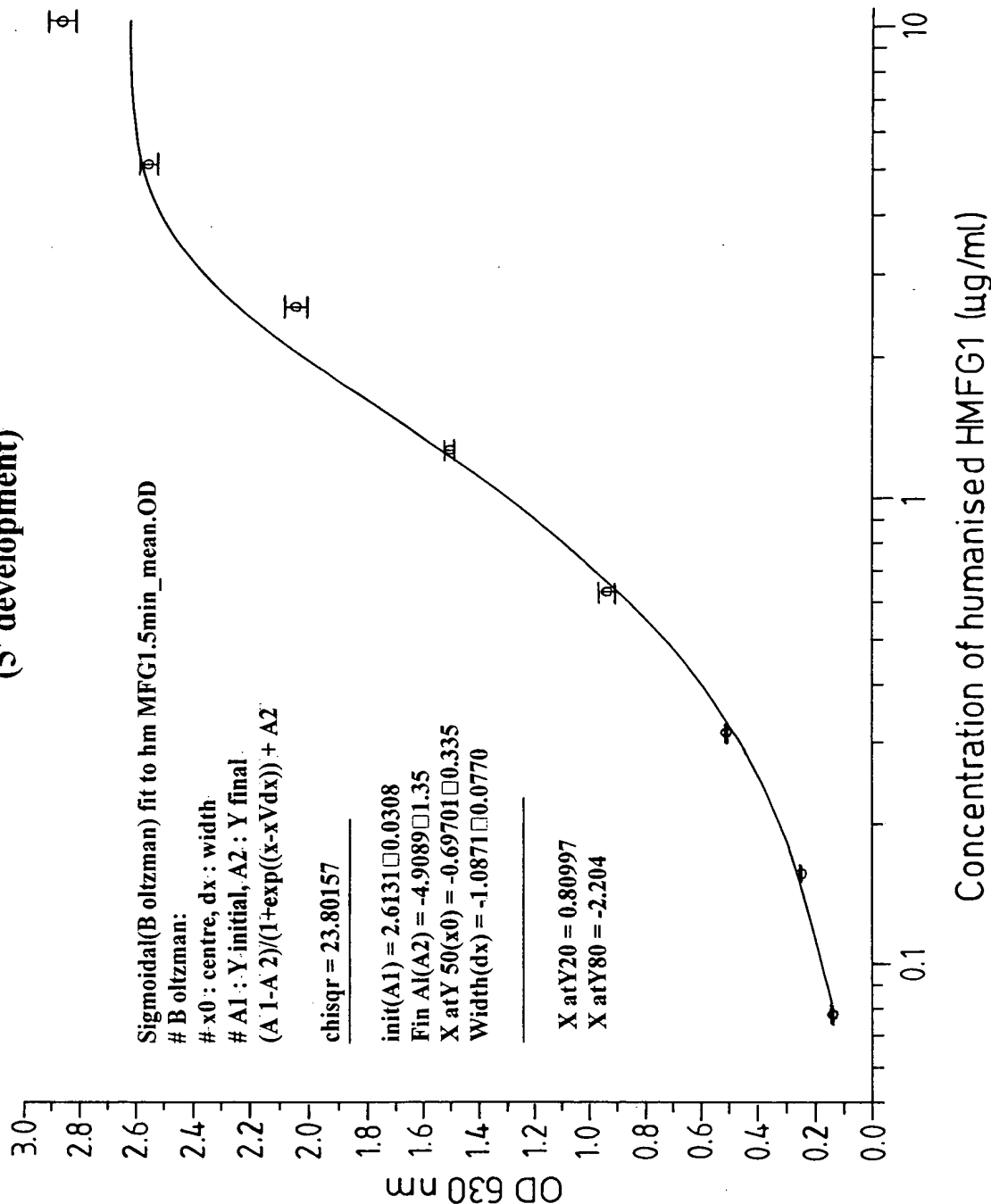
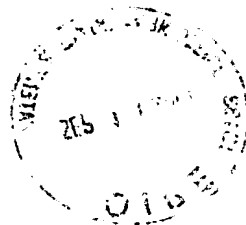
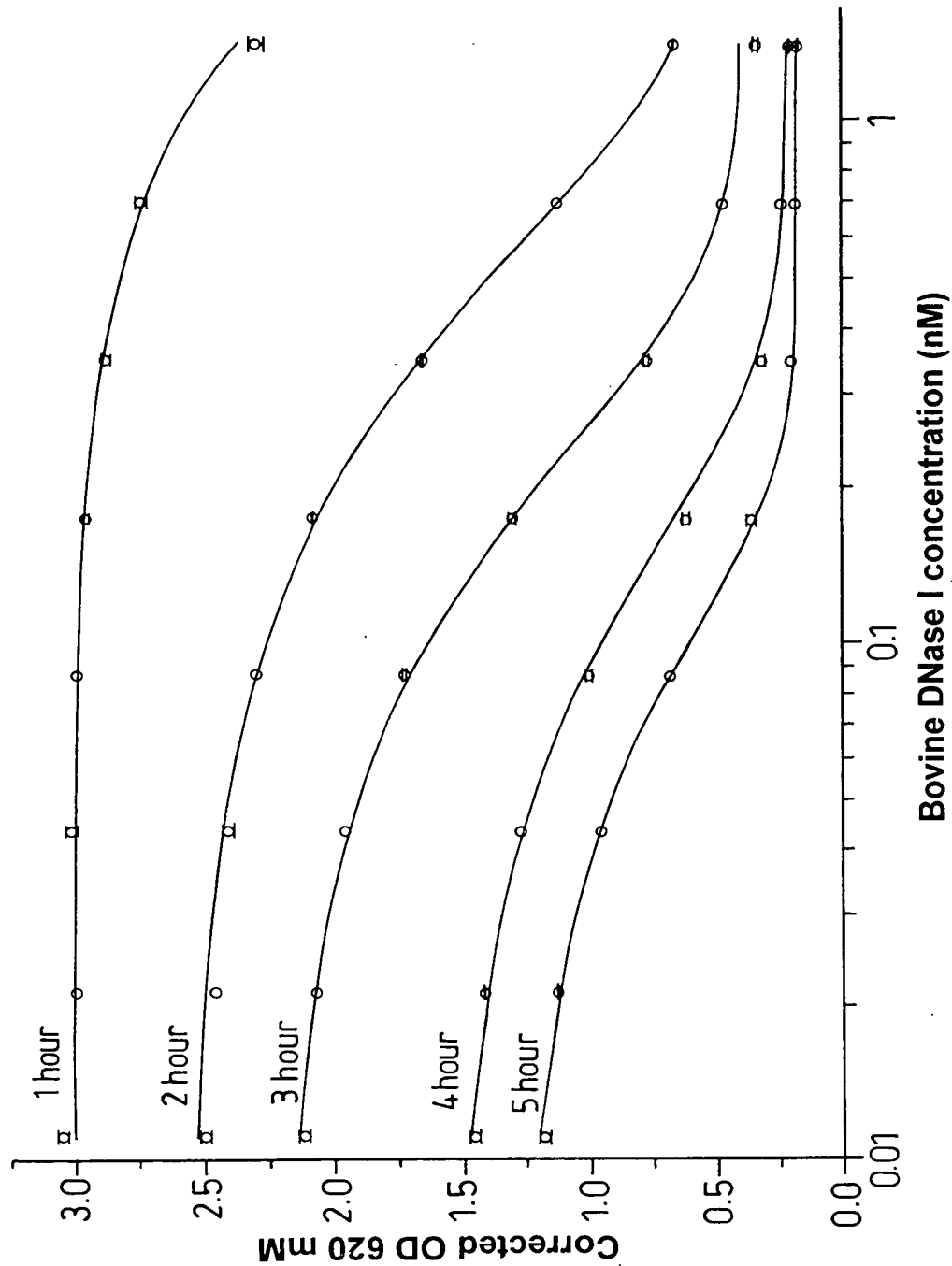


Fig. 23

Corrected bovine DNase I standard curves
at various time points



Corrected DNase I activity in transiently expressed
humanised human HMFG1-human DNase I constructs

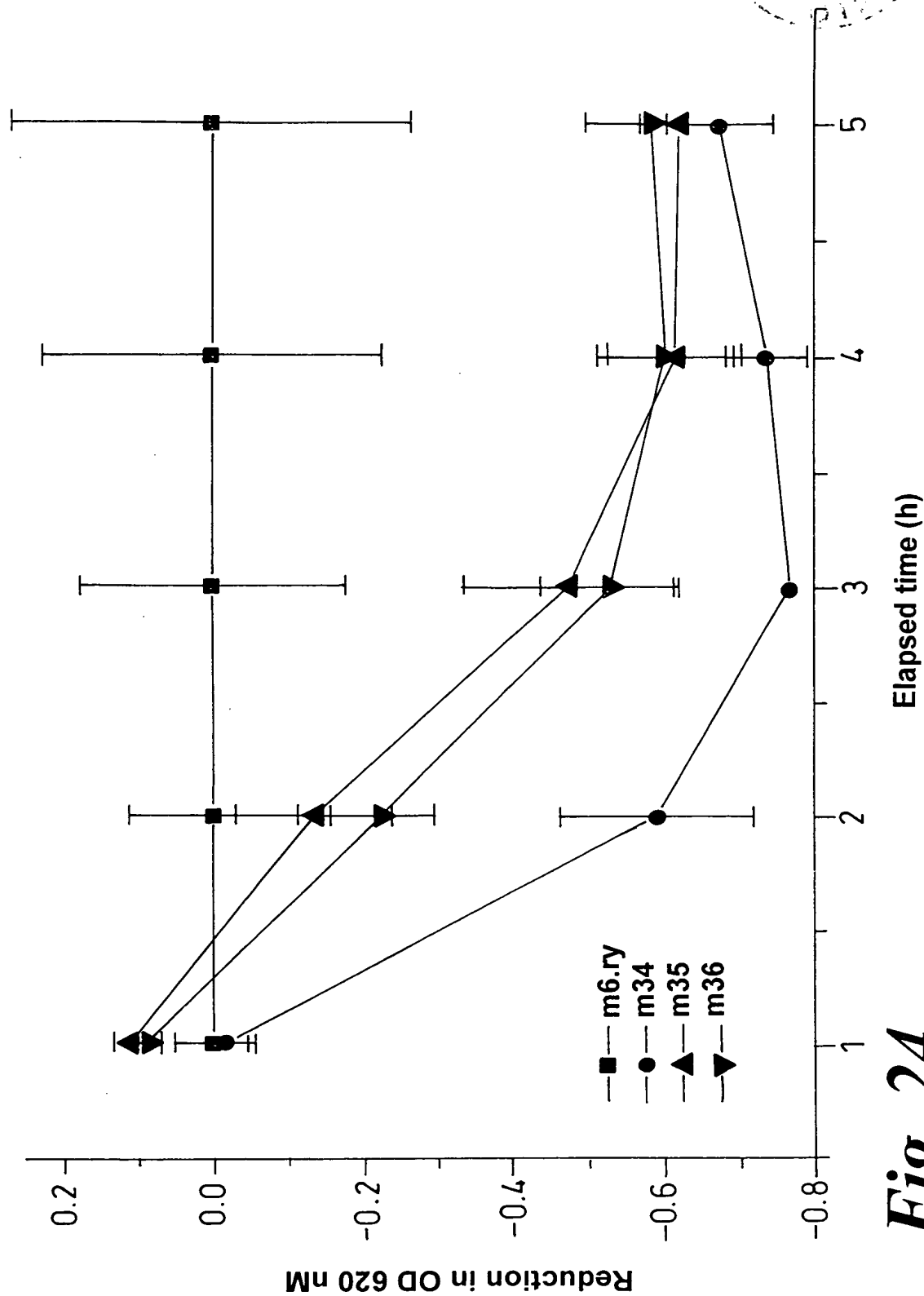


Fig. 24

Corrected DNase I activity in transiently expressed humanised HMFG1 F(ab')₂-human DNase I fusions

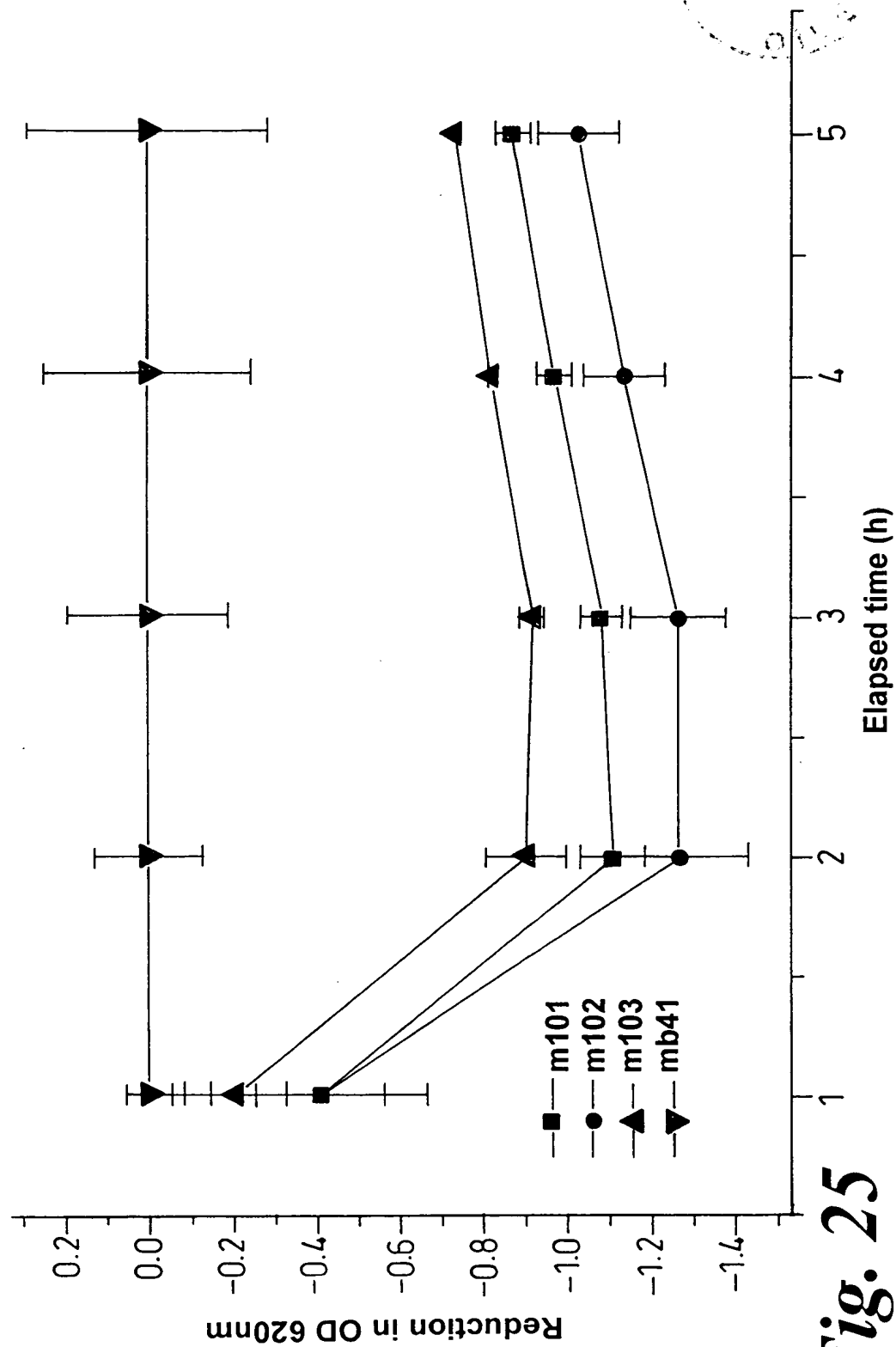


Fig. 25

Fig. 26

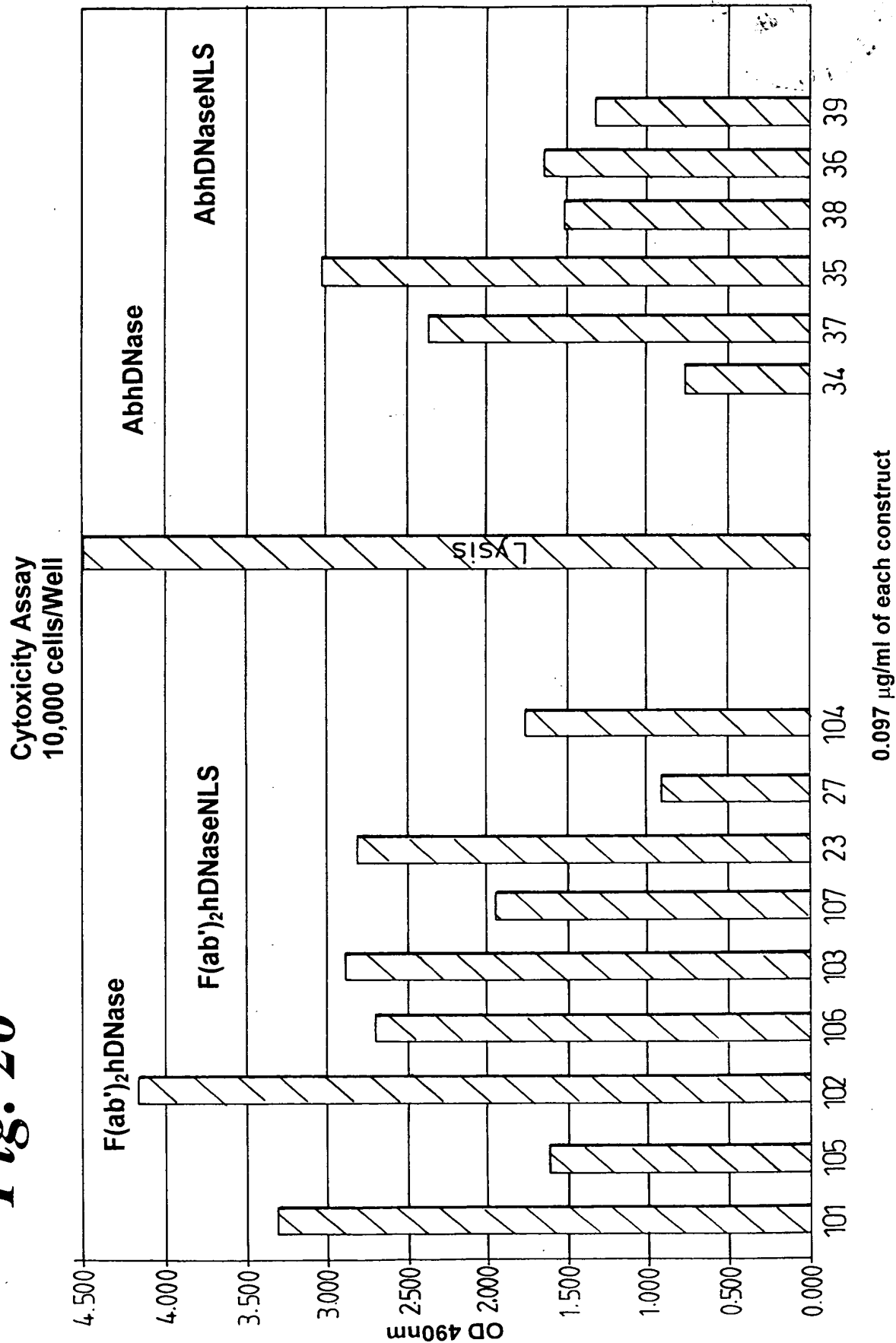
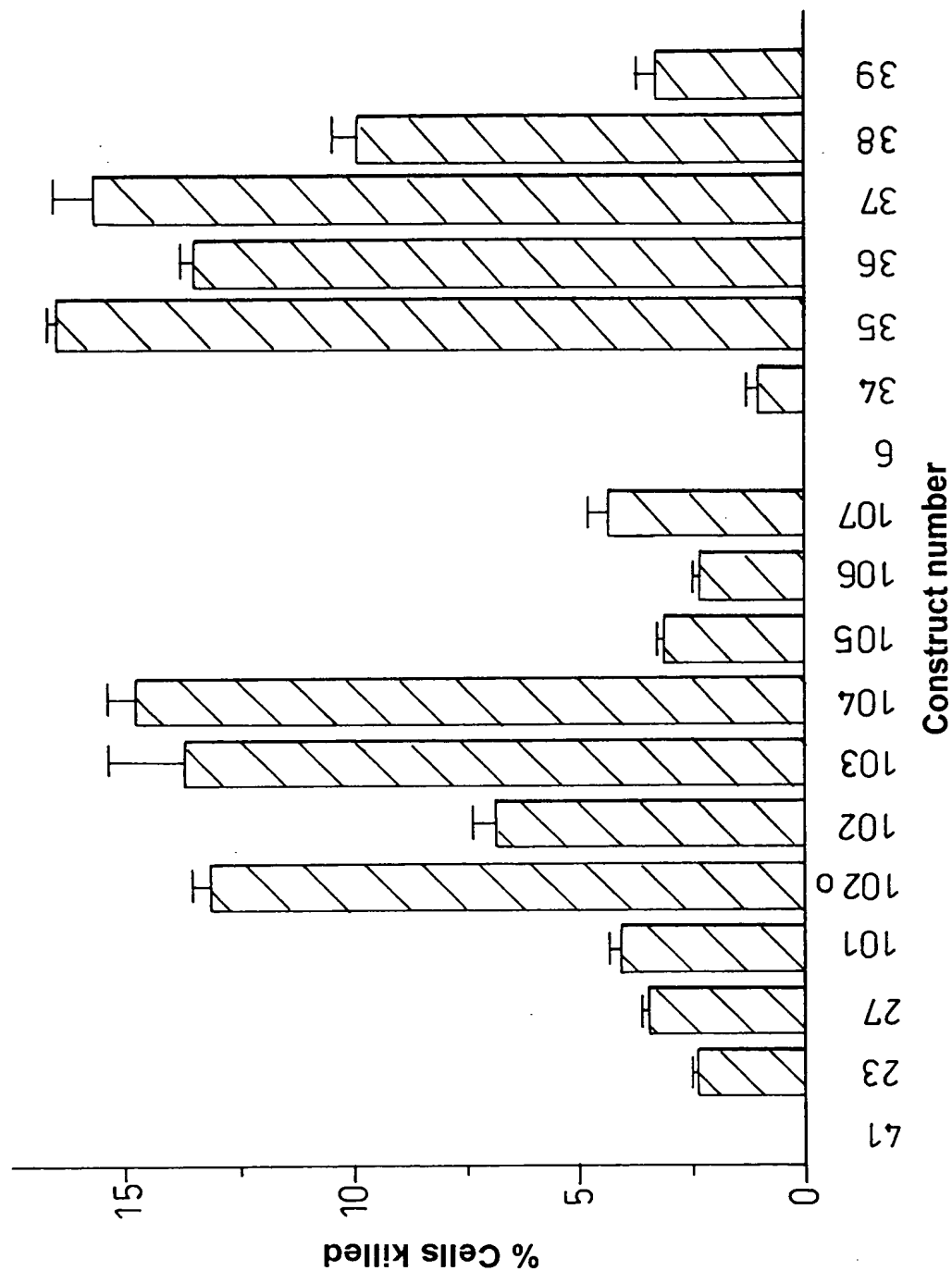


Fig. 27

MCF7 cells killed after 1h incubation with 1.35 ng of sample



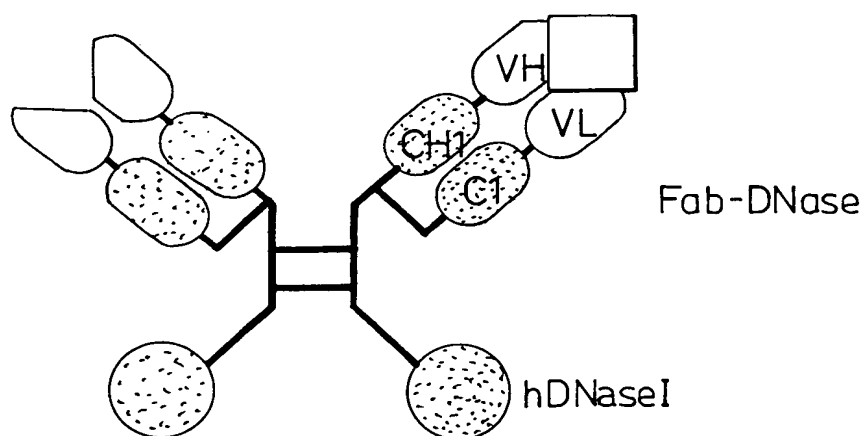
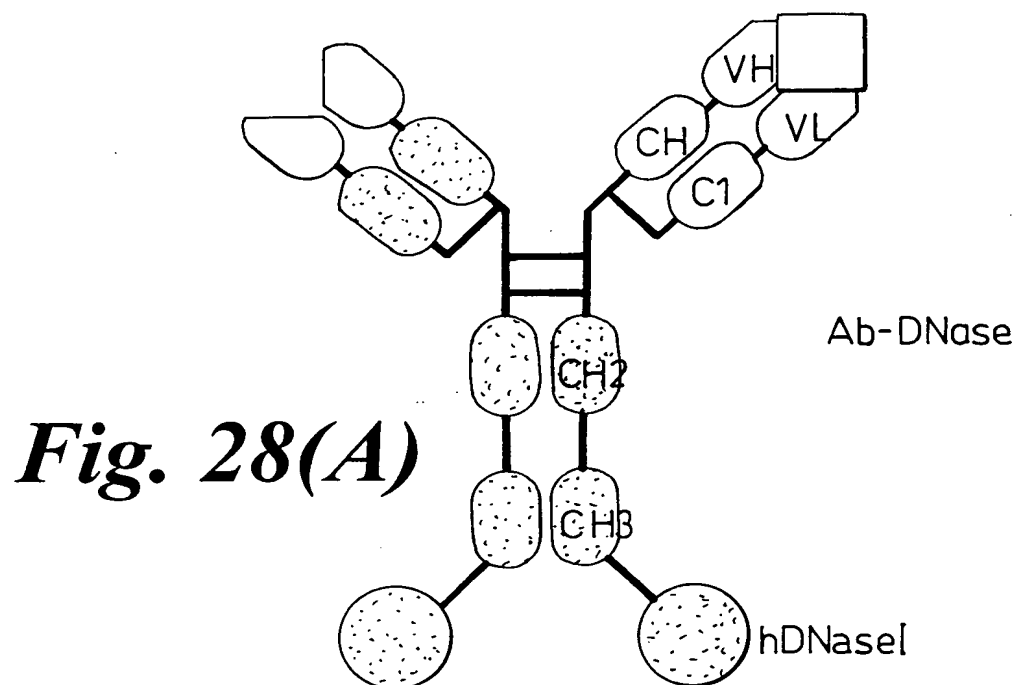
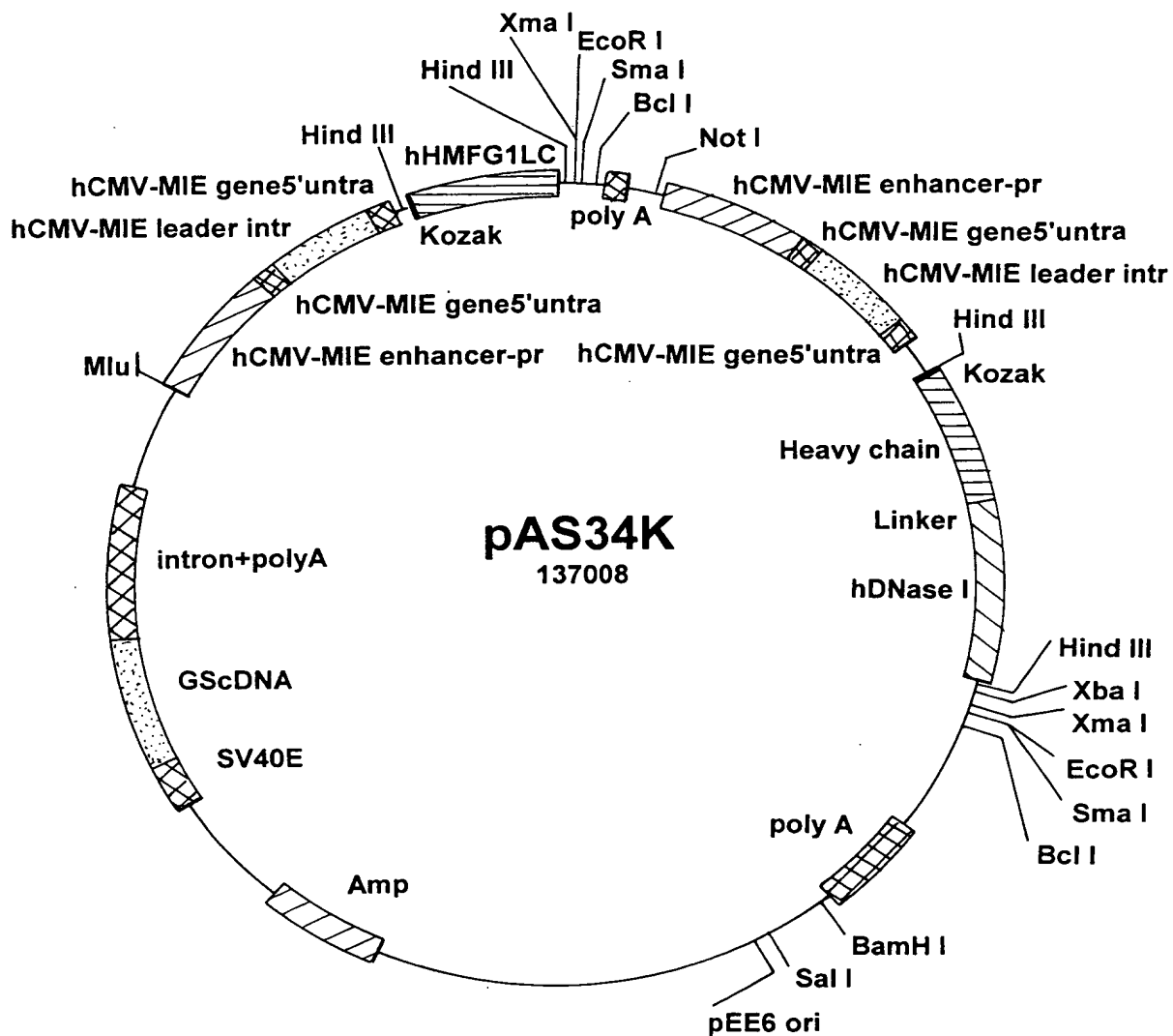


Fig. 28(B)



Ab-DNase

Fig. 29

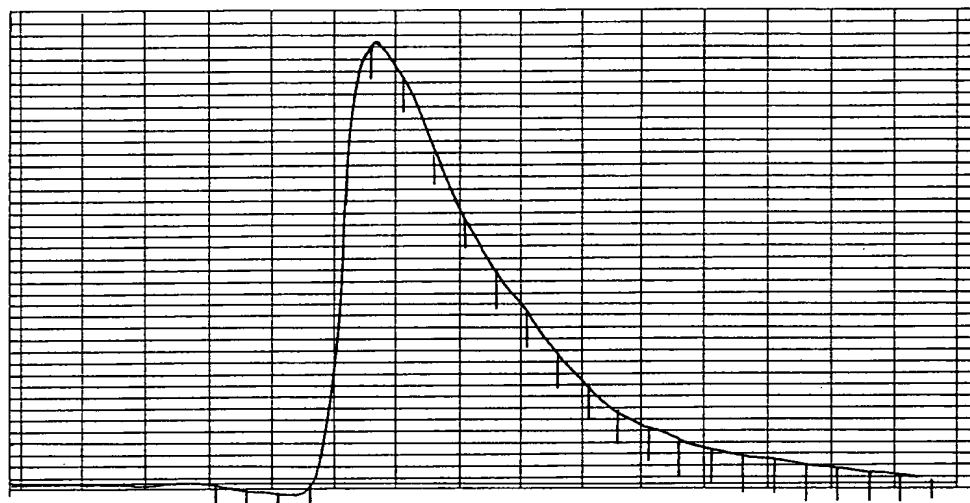


Fig. 31(A)

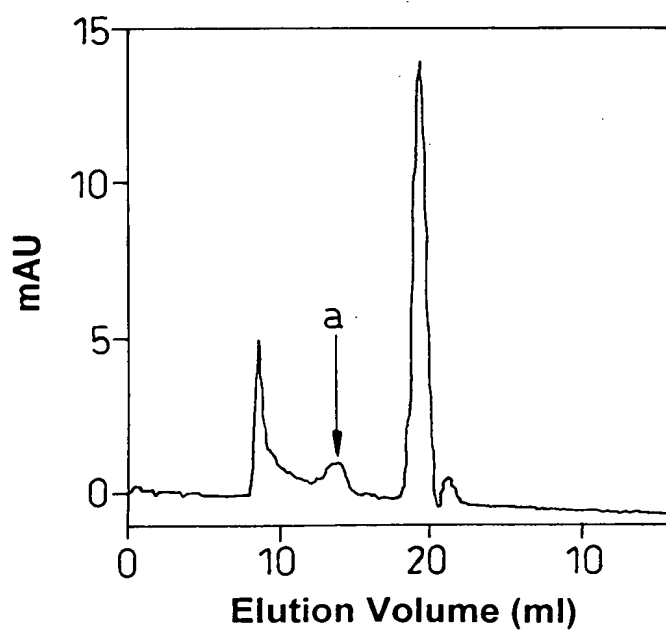
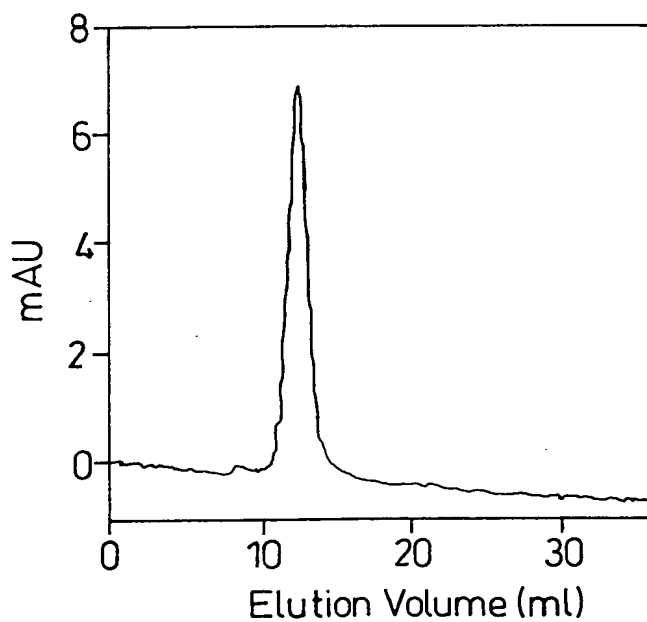
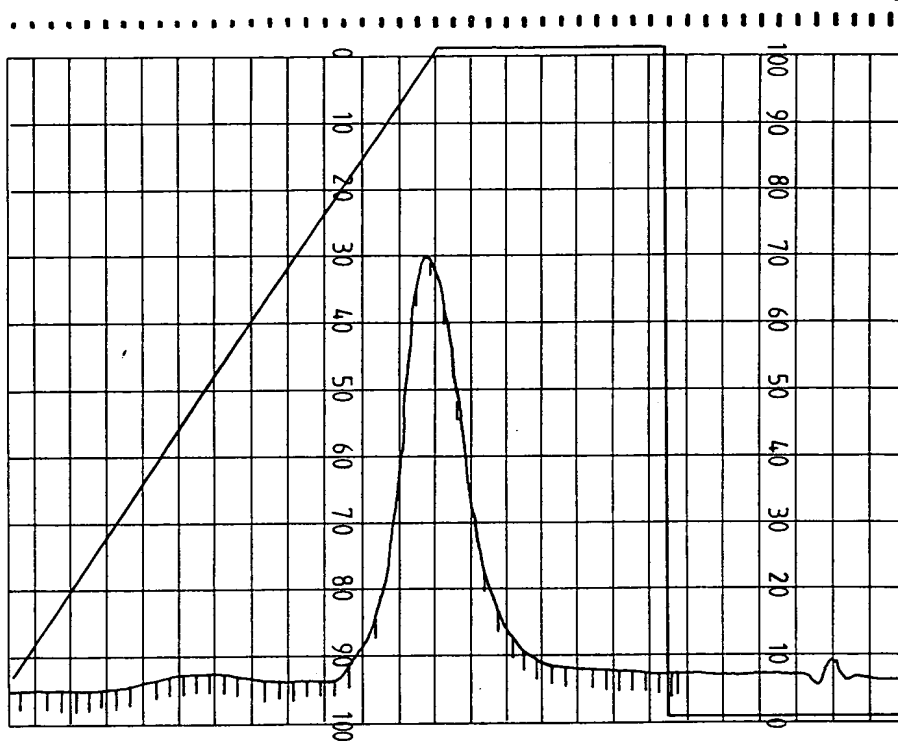


Fig. 31(B)



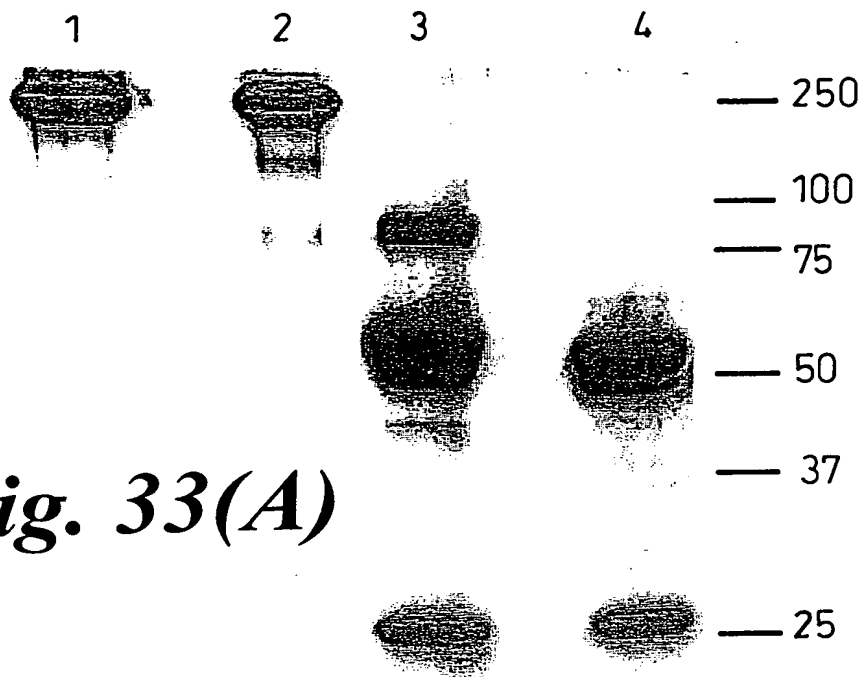
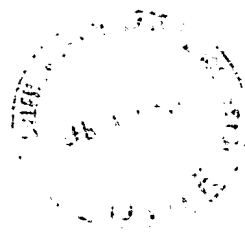


Fig. 33(A)

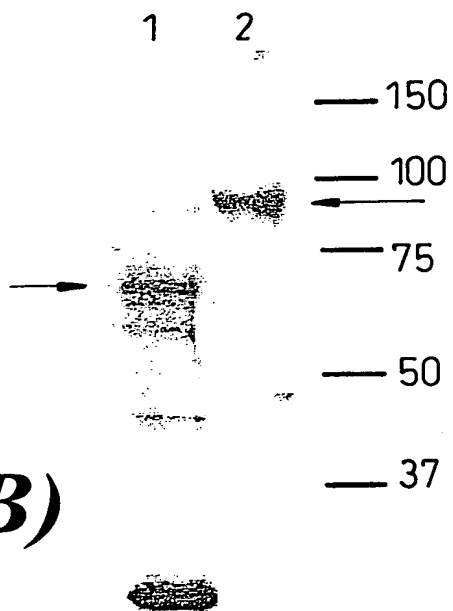
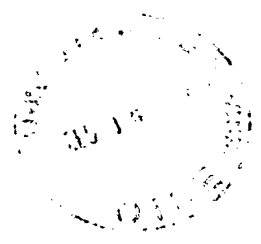


Fig. 33(B)



Bovine DNase I standard curves at various time points

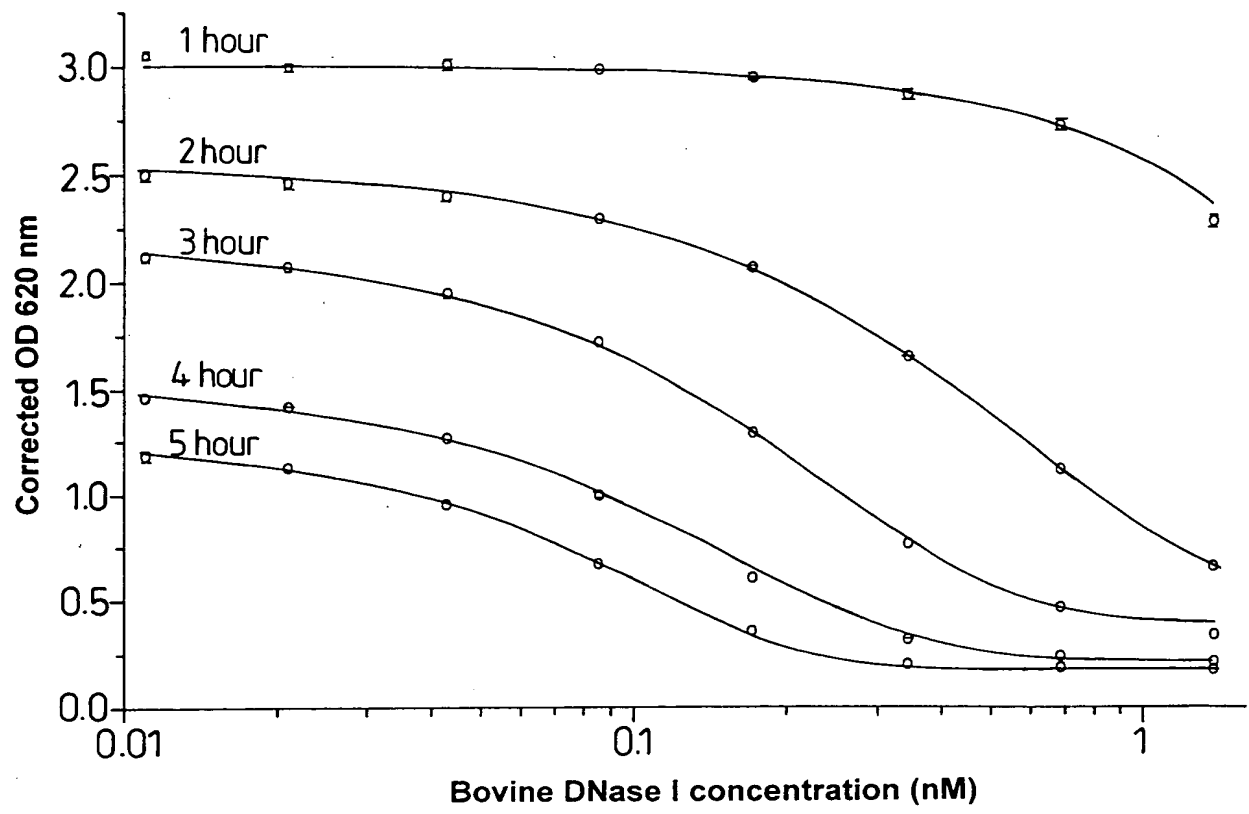


Fig. 34(A)

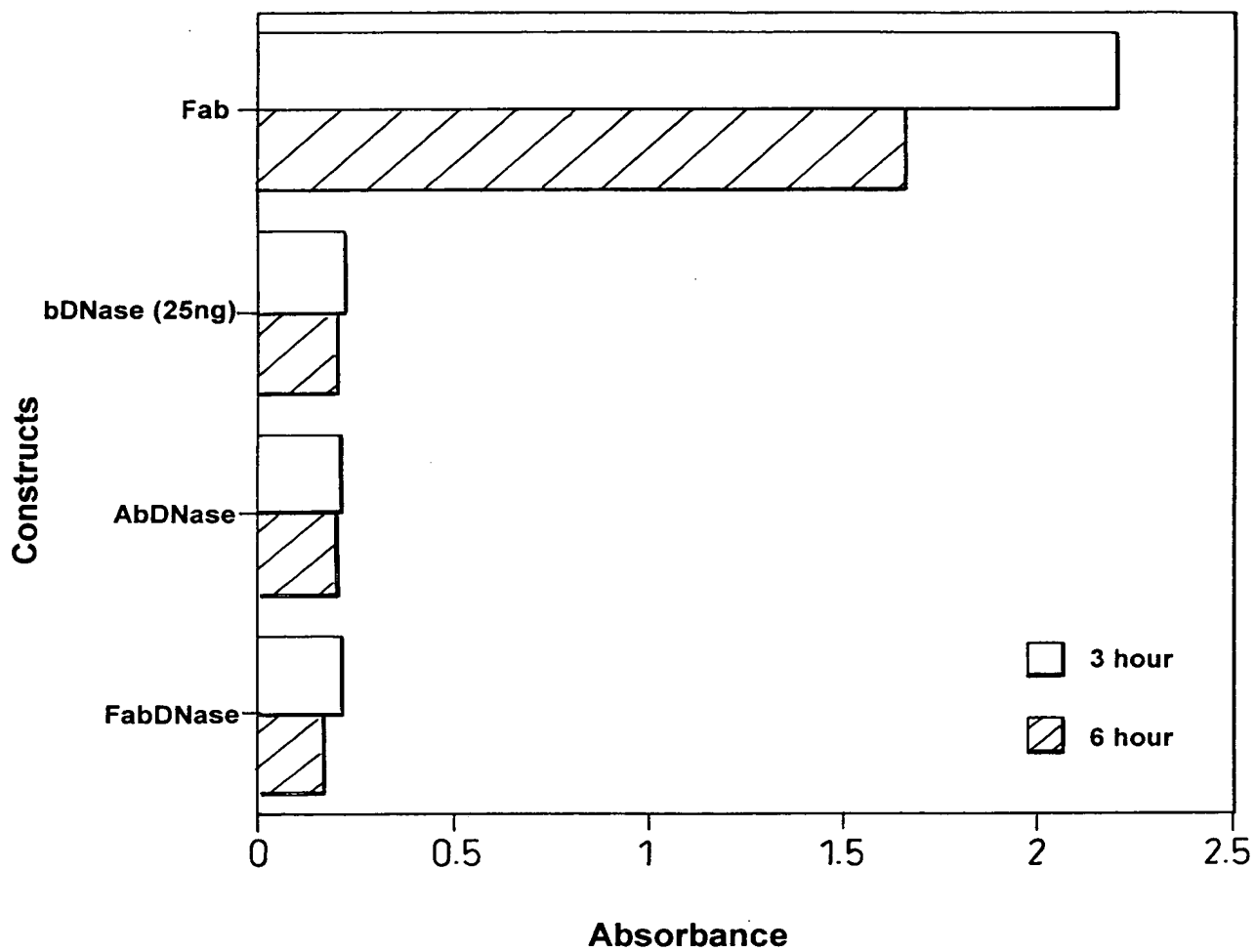


Fig. 34(B)

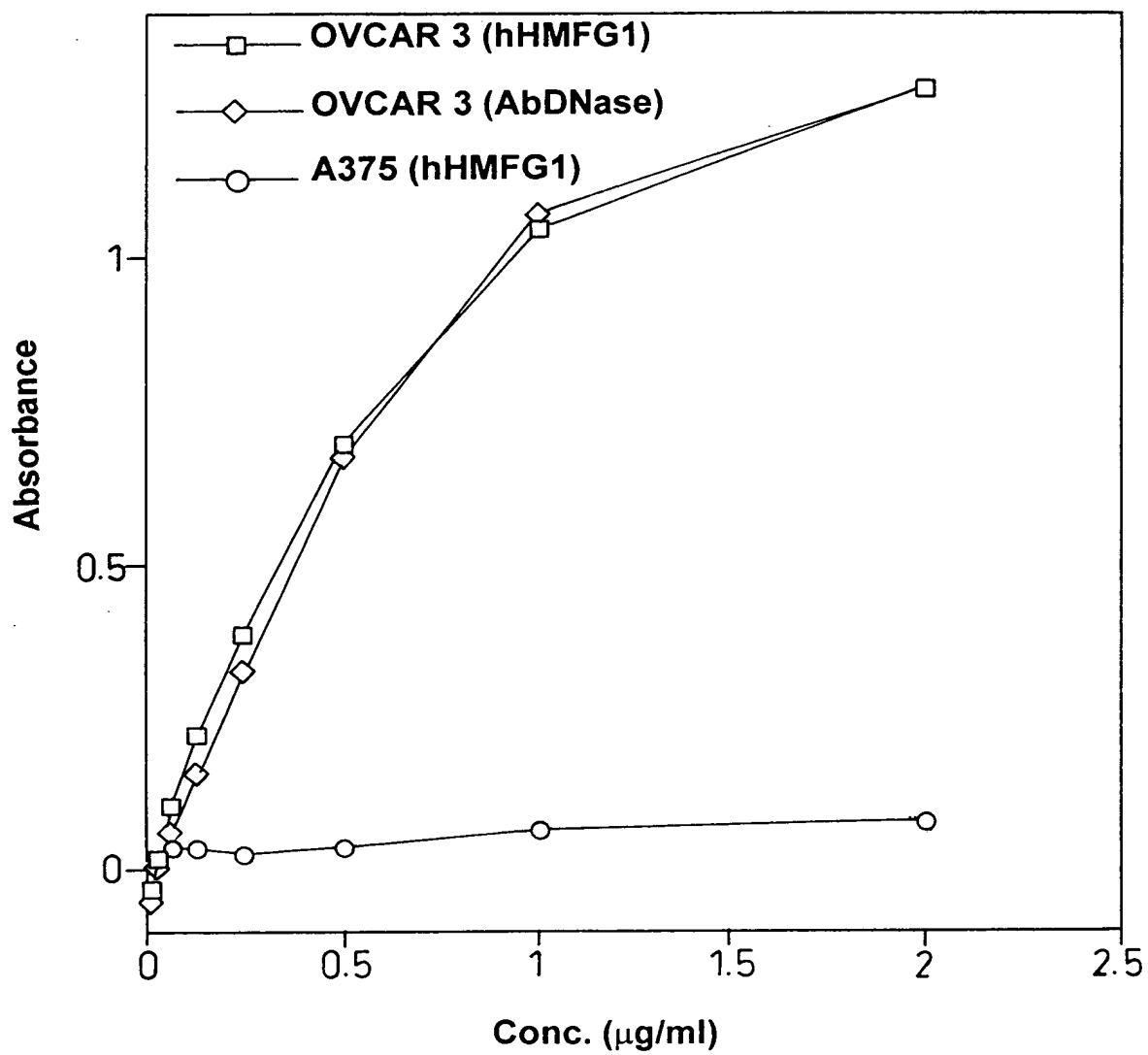


Fig. 35(A)

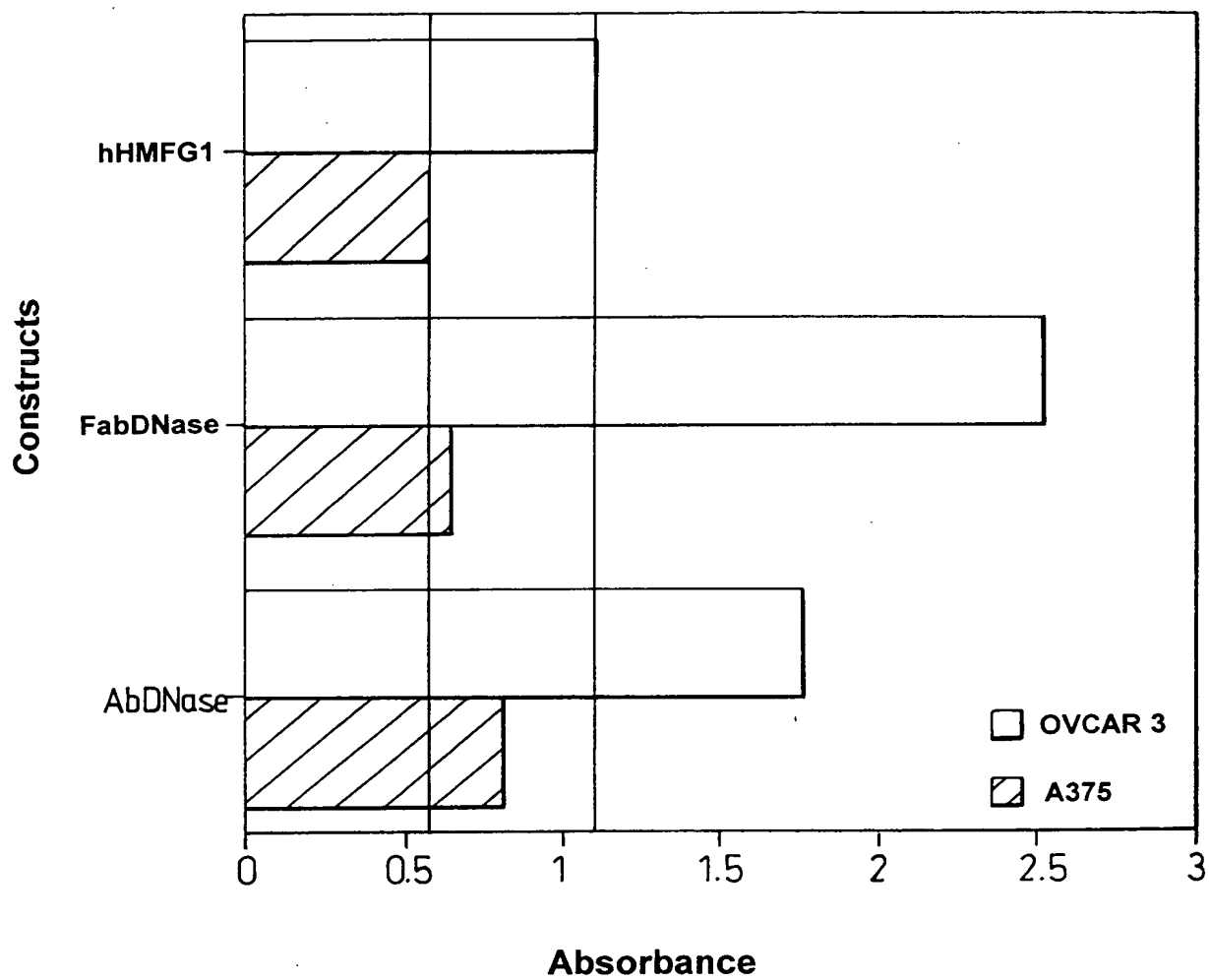


Fig. 35(B)